

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:36:27 ; Search time 1826.14 Seconds  
(without alignments)  
5638.043 Million cell updates/sec

Title: US-09-898-659-1

Perfect score: 492  
Sequence: 1 atgtatccaacgtaggata.....atgcaggcatgaccaggtga 492

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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1	307	62.4	811	8	AF261775	Lycopers1
2	298.4	60.7	821	8	AF261774	Lycopers1
3	298.4	60.7	127892	8	AF411809	Lycopers1
4	160.2	32.6	61382	8	AF411806	Lycopers1
5	123.6	25.1	683	8	AY072397	Arabidops
6	106.2	21.6	725	8	AY065153	Arabidops
7	105.6	21.5	98942	8	F24J5	Arabidops
8	95	19.3	782	8	AF049928	Arabidops
9	90.8	18.5	103550	2	AP004003	Oryza sat
10	79.2	16.1	78574	8	AP004536	Lotus jap
11	74.2	15.1	146017	2	AP003575	Oryza sat
12	73.6	15.0	132699	8	AC006917	Genomic s
13	71.6	14.6	87459	8	AB015477	Arabidops
14	71.6	14.6	89898	8	AB026658	Arabidops
15	66.8	13.6	469	8	EGU271639	Elaeis gu
16	60.4	12.3	847	8	AF327424	Arabidops
17	58.2	11.8	119091	8	AC016041	Genomic s
18	56.4	11.5	86014	8	F9C14	Sequence
19	56	11.4	46335	8	AC022354	Arabidops
20	46.8	9.5	87885	8	AC007659	Arabidops
21	45.4	9.2	975	8	AY054680	Arabidops
22	45.4	9.2	991	8	ATU78870	Arabidops
23	45	9.1	174264	2	OSJN00003	Oryza sat
24	44.4	9.0	70288	8	AC002409	Arabidops
25	41.2	8.4	407	11	G70981	Arabidops
26	40.6	8.3	1865	8	AF367322	Arabidops
27	39.6	8.0	301550	1	AP003134	Staphyloc
28	39.6	8.0	342600	1	AP003363	Staphyloc
29	38.4	7.8	168655	8	AP000969	Oryza sat
30	38	7.7	82261	2	AC066582	Homo sapi
31	38	7.7	112028	2	AC095340	Rattus no
32	38	7.7	131599	8	AC079685	Oryza sat
33	37.6	7.6	111464	8	F10K1	Sequence
34	37	7.5	6612	8	ATU78866	Arabidops
35	37	7.5	48008	8	AB025621	Arabidops
36	36.8	7.5	119420	9	HS997K18	Human DNA
37	36.8	7.5	147114	9	AP001939	Homo sapi
38	36.8	7.5	159670	2	AC027626	Homo sapi
39	36.8	7.5	159960	2	AC098620	Rattus no
40	36.8	7.5	164229	9	AC092671	Homo sapi
41	36.8	7.5	183680	9	AC098859	Homo sapi
42	36.8	7.5	269081	2	AC068493	Mus muscu
43	36.6	7.4	101944	9	AC011463	Homo sapi
44	36.6	7.4	193683	2	AC011590	Homo sapi
45	36.4	7.4	392	11	G71820	Arabidops

ALIGNMENTS

RESULT 1  
AF261775  
LOCUS AF261775 811 bp DNA linear PLN 06-JUN-2000  
DEFINITION Lycopersicon pennellii ORFX (ORFX) gene, complete cds.  
ACCESSION AF261775.1 GI:8272627  
VERSION  
KEYWORDS  
SOURCE Lycopersicon pennellii.  
ORGANISM Lycopersicon pennellii.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 811)  
Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der  
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and  
Tanksley,S.D.  
fw2.2: a quantitative trait locus key to the evolution of tomato  
fruit size  
Unpublished  
2 (bases 1 to 811)  
Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der  
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and

Printed

Tanksley, S.D.  
Direct Submission  
Submitted (28-APR-2000) Plant Breeding, Cornell University, 248  
Emerson Hall, Ithaca, NY 14853, USA

FEATURES  
Source 1..811  
/organism="Lycopersicon pennellii"  
/db\_xref="taxon:28526"  
/notes="fw2.2; small-fruit"  
join(55..262,365..574,644..717)  
/gene="ORFX"  
/product="ORFX"  
55..717  
/gene="ORFX"  
/notes="ORFX"  
/codon\_start=1  
/product="ORFX"  
/protein\_id="AAF74287.1"  
/db\_xref="GI:8272628"  
/translation="MPTPYGYNGLMKQYPVPPHYVAPGTTTARWSTGLCHCFDDPA  
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DLIEAPVCDLVHFCPEALCQYRELKRGFDGMIGWQANMDRQSRGVTPPYHAG  
MTR"

BASE COUNT 221 a 138 c 169 g 283 t

ORIGIN

Query Match 62.4%; Score 307; DB 8; Length 811;  
Best Local Similarity 80.4%; Pred. No. 7.5e-71;  
Matches 419; Conservative 0; Mismatches 0; Indels 102; Gaps 1;

QY 1 atgtatccacgtagatataatcttaggtctaatgaacacaccttatgtctcctcac 60  
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DB 55 ATGTATCCACGGTAGATATAATVCTAGGTCTAATGAACAACCTTAATGTCTCTCCAC 114  
|||||  
QY 61 tatgtatctgccccgcacacacccagcgcggtgggtcaactggtctttgcactgttt 120  
|||||  
DB 115 TATGTATCTGCCCGCACACACACGCGGGTCAACTGGTCTTTGTCACGTGTTT 174  
|||||  
QY 121 gatgacctgtaactgttagttactagtgtttgcccttgatcacaccttggacagatt 180  
|||||  
DB 175 GATGACCCCTGCTAACTGTTTAGTTACTAGTGTGTTGCCCTTGTATCACCTTTGGACAGATT 234  
|||||  
QY 181 tctgaatactaaacaaggaacaactt----- 208  
|||||  
DB 235 TCTGAATATCTAACAAAGGACAACTGTGAAGTATATATATACACATCTCTTTTTTTT 294  
|||||  
QY 209 ----- 208  
DB 295 GGGATAAGTTCAATTTATTTGGTTACCAAGAATATGATGTTGTGCTGTTTTTC 354  
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QY 209 -----catgtggagtagagtgcatattatgttctgtggactgacagattg 258  
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DB 355 TTGATGTTAGCACTGGGAGTAGAGGTGCATATATTGTTGCTGGAGCTGCACAGATTG 414  
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QY 259 cctgagcctatattcctgctcttacaggtctctaaatgagggggcaatatgatcttggaaag 318  
|||||  
DB 415 CCTAGCCTATATTCCTGCTCTACAGCTCTAAAAATGAGGGGCAATATGATCTGGAAGAG 474  
|||||  
QY 319 qcacctgtgtgattgctctgtacatgattctctgtaacctgtgctcttggccaagaa 378  
|||||  
DB 475 GCACCTGTGTGATTGCTTGTACATGTAFTCTGTAACCTTGTGCTCTTTGCCAAGAA 534  
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QY 379 tacagagcgttaagaaccgtggcttggatgggaatagg 419  
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DB 535 TACAGAGAGCTTAAGAACCGTGGCTTTGATATGGAATAGG 575  
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RESULT 2  
AF261774  
LOCUS AF261774 821 bp DNA linear PLN 06-JUN-2000

DEFINITION	Lycopersicon esculentum ORFX (ORFX) gene, complete cds.				
ACCESSION	AF261774				
VERSION	AF261774.1 GI:8272625				
KEYWORDS	tomato.				
SOURCE	Lycopersicon esculentum				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.				
REFERENCE	1 (bases 1 to 821)				
AUTHORS	Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and Tanksley,S.D.				
TITLE	fw2.2: a quantitative trait locus key to the evolution of tomato fruit size				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 821)				
AUTHORS	Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and Tanksley,S.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-APR-2000) Plant Breeding, Cornell University, 248 Emerson Hall, Ithaca, NY 14853, USA				
FEATURES	Location/Qualifiers				
source	1..821				
	/organism="Lycopersicon esculentum"				
	/db_xref="taxon:4081"				
	/notes="fw2.2: large-fruit"				
mRNA	join(56)..263,365..574,653..726)				
	/gene="ORFX"				
gene	/product="ORFX"				
	56..726				
	/gene="ORFX"				
CDS	join(56)..263,365..574,653..726)				
	/gene="ORFX"				
	/note="LeORFX"				
	/codon_start=1				
	/product="ORFX"				
	/protein_id="AAF74286.1"				
	/db_xref="GI:8272626"				
	/translation="MYQTGYNPGPMKPQVPPHYVSAPGTTTARWSTGLCHCFDDPA NCLVTSVCPINFGOISEIILNKGTTCGSRGALYCLLGLTLPGLPSLYSCFVRKMRGOY DUEEAPCVCLVHVFCPEPCALCOEYRELNRGFDMDIGHQANDRQSRGVTHPPYHAG MTR"				
BASE COUNT	224 a	138 c	177 g	282 t	
ORIGIN					
Query Match	60.7%; Score 298.4; DB 8; Length 821;				
Best Local Similarity	79.4%; Pred. No. 1.4e-68;				
Matches 413; Conservative	0; Mismatches	6; Indels	101; Gaps	1;	
Qy	1	atgtatccaacggtaggatataatcttaggtctaattgaacaaaccttatgttccctccac	60		
Db	56	ATGTATCAACGGTAGATATATATCCAGGTCCAATGAACAACCTTATGTTCCTCCTCAC	115		
Qy	61	tatgtatctgccccccgcacacacacacgcgcggttggtcaactggcttbtgcactgtttt	120		
Db	116	TATGTATCTGCCCGCGACACACACCGCGCGGTGTCGACTGTGCTCTTGTCAATGTGTTT	175		
Qy	121	gatgacctgtaactgttttagttactagtgtttgccttggatcaccttggacagatt	180		
Db	176	GATGACCTGTCACTACTGTTTAGTTTACTAGTGTGTTGGCCCTTGATCACCTTTGGACATT	235		
Qy	181	tctgaataactaaacaaggaacaactt-----	208		
Db	236	TCTGAATACTAAACAAGGAACAACCTGTGAAGTATATACACTTTTTTTTGGGGGGGG	295		
Qy	209	-----	208		
Db	296	GGATAAATTCAATTTATTTGATATTTGGTTACCAAGAATATGATGTTGTGTTGTTTCT	355		

2  
RESULT  
AF261774  
LOCUS

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QY 209 -----catgtgggagtagagtgcatattattgttctgggactgcacagattgc 259
Db 356 TGATGTTAGCATGTGGGAGTAGAGTGCAATTATATTGTTGCTGGGATTTGACAGATTGC 415
QY 260 ctagcctatatcttctctcacaggtctaaataagaggggcaaatatgatctggaagagg 319
Db 416 CTAGCCTATATTCCTGCTCTACAGGTCTAAATGAGGGGCAATATGATCTGGAAGAGG 475
QY 320 caccctgtgtgatgtctctgtacatgtattctgtgaacctgtgtctctttgccagaat 379
Db 476 CACCTGTGTGATGTTCTGTACATGATATCTGTGAACCTGTGCTCTTTGCCAAGAAAT 535
QY 380 acagagagcttaagaacctggtctttgatgggaatagg 419
Db 536 ACAGAGAGCTTAAGAACCGTGGCTTTGATATGGGAATAGG 575

RESULT 3
AF411809/c 127892 bp DNA linear PLN 07-OCT-2001
LOCUS Lycopersicon esculentum BAC clone FW2.2, complete sequence.
DEFINITION AF411809
ACCESSION AF411809
VERSION AF411809.1 GI:15987774
KEYWORDS tomato.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 127892)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE Deductions about the number, organization and evolution of genes in
the tomato genome based on analysis of large EST collection and
selective genomic sequencing
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 127892)
AUTHORS Nesbitt,C.T., van der Hoeven,R.S. and Tanksley,S.D.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-2001) Plant Breeding, Cornell University, 252
Emerson Hall, Ithaca, NY 14850, USA
FEATURES
source
1..127892
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone="FW2.2 BAC"
BASE COUNT 42761 a 20070 c 20496 g 44565 t
ORIGIN

Query Match 60.7%; Score 298.4; DB 8; Length 127892;
Best Local Similarity 79.4%; Pred. No. 7.2e-69;
Matches 413; Conservative 0; Mismatches 6; Indels 101; Gaps 1;

QY 1 atgtatccaacggtaggatataatctaggtctaataagaacaccttatgttctctctcac 60
Db 19179 ATGTATCAAAACGTTAGGATATAATCAGGTCCAATGAACCAACCTTATGTTCTCTCTCAC 19120
QY 61 tatgtatctgccccggcaccacacacgcgcggtgtgtcaactggtctttgtcaactgtttt 120
Db 19119 TATGTATCTGCCCCGGCACACCACCGCGGTGTGTGCGATGCGTCTTTGTGTCATTTGTTT 19060
QY 121 gatgacctgctaactgttttagttactagtgtttgcccttgtatcaccttttgacagatt 180
Db 19059 GATGACCTTGCTAACTGTTTACTGTACTGTGTTGCCCTTGTATCACCTTTGGACAGATT 19000
QY 181 tctgaataactaacaagaaggaaacctt----- 208
Db 18999 TCTGAATAACTAAACAAGGAACAACCTTCTGAAGTATATACACTTTTTTTTTTGGGGGGGG 18940
QY 209 ----- 208
Db 18939 GGATAAATCAATTTATTGATATTGGTTACCAAGAATATGATGTTTGTGTTTCT 18880
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QY 209 -----catgtgggagtagagtgcatattattgttctgggactgcacagattgc 259
Db 18879 TGATGTTAGCATGTGGGAGTAGAGTGCAATTATATTGTTGCTGGGATTTGACAGATTGC 18820
QY 260 ctagcctatatcttctctcacaggtctaaataagaggggcaaatatgatctggaagagg 319
Db 18819 CTAGCCTATATTCCTGCTCTACAGGTCTAAATGAGGGGCAATATGATCTGGAAGAGG 18760
QY 320 caccctgtgtgatgtctctgtacatgtattctgtgaacctgtgtctctttgccagaat 379
Db 18759 CACCTGTGTGATGTTCTGTACATGATATCTGTGAACCTGTGCTCTTTGCCAAGAAAT 18700
QY 380 acagagagcttaagaacctggtctttgatgggaatagg 419
Db 18699 ACAGAGAGCTTAAGAACCGTGGCTTTGATATGGGAATAGG 18660

RESULT 4
AF411806 61382 bp DNA linear PLN 07-OCT-2001
LOCUS Lycopersicon esculentum BAC clone Clemson_Id 207, partial sequence.
DEFINITION AF411806
ACCESSION AF411806
VERSION AF411806.1 GI:15987771
KEYWORDS tomato.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 61382)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE Deductions about the number, organization and evolution of genes in
the tomato genome based on analysis of large EST collection and
selective genomic sequencing
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 61382)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-2001) Plant Breeding, Cornell University, 252
Emerson Hall, Ithaca, NY 14850, USA
FEATURES
source
1..61382
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone="Clemson_Id 207 BAC"
/note="fragment 2"
BASE COUNT 20121 a 11562 c 10377 g 19322 t
ORIGIN

Query Match 32.6%; Score 160.2; DB 8; Length 61382;
Best Local Similarity 90.6%; Pred. No. 3.2e-32;
Matches 193; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 209 catgtgggagtagagtgcatattattgttctgggactgcacagattgcctaccta 267
Db 21362 CATGTGCTAGTAGAGGTGCATTTATGTTGTTGGGACTGAACAGGATTCCTTACCTTA 21421
QY 268 tattctctctctcacaggtctaaataagaggggcaaatatgatctggaagagcaccttgt 327
Db 21422 TATTCCTACTTCTATAGGTCCAAATGAGAGGCAATGTGATCTGGAAGAGCACCTTGT 21481
QY 328 gttgattgtcttgtaca-tgtattctgtgaacctgtgtctctttgccagaatacacaga 386
Db 21482 GCGGATTGCTTGAACATTTGATTCTGTGAACCTTGTGCTCTTATCCAAGAGACAGAGA 21541
QY 387 gcttaagaacctggtctttgatagggaatagg 419
Db 21542 GCTTAAGAACCTTGCTTTAATATATGGGAATAGG 21574
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cDS      125..526
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/codon_start=1
/product="unknown protein"
/protein_id="AAL38329.1"
/db_xref="GI:17473788"
/translaton="MEKOWTSGFLSCMEDSETACLTFCPCVTFGRADISDEGRTCG
GRGVFGLICCVVGLPCLFSCYTRTKRSKFGLPSPESPTSDCVTHFFCECCALCQHR
ELKTRGLDPSIGSGNMQRTMAPPMQOMMG"
BASE COUNT      217 a 131 c 152 g 225 t
ORIGIN

Query Match      21.6%; Score 106.2; DB 8; Length 725;
Best Local Similarity 58.4%; Pred. No. 1.2e-17;
Matches 205; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

Qy 90 gcggtggtcaactggctttgtcaactgttttgatgacacctgctaaactgttagttactag 149
Dy 133 GCAATGGACTTCTGGCTCTTTTCAGCTGCATGGAGACAGTGAACACTGCTTGCCTCACATG 192
Qy 150 tgtttgacctgtatcaccttggacagatcttgaataactaaacaagaacaacttc 209
Dy 193 TTTCTGCCCATCGCTCACTTTCCGACGATCGCGACATTTCCGACGAGGAAGACCGG 252
Qy 210 atgtgggagtagtgatgatttattgttct---gggactgacaggattgcctagcct 266
Dy 253 TTGTGGGAGATGTGGGTATTTACGGGCTAATATGTTGTGTGGTGGCTTACCTTGCTT 312
Qy 267 atattcgtcttcaacagttcaaatgaggggcaaatatgatctggaaggagcaacttg 326
Dy 313 GTTCTCACTGCACTTACCGGACCAAGATCCGAAGCAAAATTCGGGTTACCGGATCTCCAAC 372
Qy 327 tgtgattgctcttgacatgattctgtgaaccttgcctcttcttgcgaagaatacagaga 386
Dy 373 TTCGATGCGCTCACTCACTCTTTTGTGTAATGTGTGCTCTTTCGCAAGAACCCGTGA 432
Qy 387 gcttaagaacctggcttgatggaatagggtgggcaagtataatagga 437
Dy 433 ACTCAAAACCGGTGCTCTTGACCCCTCTATTGGGTGGAGTGGAATATGCA 483

RESULT 7
F24J5/c
LOCUS      Arabidopsis thaliana chromosome 1 BAC F24J5 sequence, complete
DEFINITION
ACCESSION      AC008075
VERSION      AC008075.2 GI:5724802
KEYWORDS      HTG.
SOURCE      thale cress.
ORGANISM      Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 98942)
Vysotskaia,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S.,
Lee,J.M., Li,J., Gonzalez,A., Liu,A., Liu,K., Vaysberg,M.,
Sakano,H., Chin,C., Choi,E., Chlou,J., Altafi,H., Araujo,R.,
Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Dunn,P.,
Hansen,N., Howng,B., Huizar,L., Khan,S., Kim,C., Palm,C.,
Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R.,
Fedorisiel,N.A. and Theologis,A.
The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1
Unpublished
2 (bases 1 to 98942)
Theologis,A.
Direct Submission
Submitted (19-JUL-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 98942)
Theologis,A.
Direct Submission

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Submitted (10-AUG-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 98942)
Theologis,A.
Direct Submission
Submitted (17-AUG-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
On Aug 10, 1999 this sequence version replaced gi:5525042.
The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.
Location/Qualifiers
1..98942
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
/clone="F24J5"
1121..6282
/gene="F24J5.1"
join(1121..1276,1432..1595,1764..1821,1940..2017,
2103..2171,2251..2329,2407..2483,2575..2713,2899..3039,
3364..3386,3492..3728,3827..3952,4035..4136,4212..4358,
4459..4557,4638..4726,4847..4973,5048..5254,5458..6282)
/gene="F24J5.1"
/note="Similar to gblX90982 phosphoenolpyruvate
carboxylase (ppcl) from Solanum tuberosum."
/codon_start=1
/evidence=not_experimental
/protein_id="AADA9968.1"
/db_xref="GI:5734703"
/translaton="MTDTDDIAEEISFQFEDDCKLGLSFHDVLQREVNPPMEKV
ERIRLAQSALNRMAGIEDTANLEKQLTSEISKMPLEALTARTTSHSLNMGIA
DTHSOLLQSGISPELYKTVCKQEVILVTAHPTQINRRTLOVKHTRIAHLLEYNTR
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RVNSNLSKKTGKPLCTCPKMGEGSGMDGDNPNVAKYSLILYDLNSKTGHE
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GSAPYRIVLGEVKLTKRLLELLEGLPEYDKNYSSTQDLLELLYSQESLQ
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join(12650..13268,13470..14071,14223..14352,14653..14780,
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/note="Contains similarity to gblAF14753 polytropic
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EST gblN96331 comes from this gene."
/codon_start=1
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TIOY"  
complement(20404. .24677)  
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CDS  
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/gene="F24J5.5"  
/note="Contains similarity to gl13293316 cytosine  
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and contains a PF100383 cytidine deaminase zinc-binding  
region. EST gb1W43306 comes from this gene."  
/codon\_start=1  
/evidence=not\_experimental  
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/db\_xref="GI:5734706"  
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33736. .33824,33936. .34044,34142. .34345,34427. .34552,  
34645. .34743,34827. .35018,35097. .35726)  
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/note="Similar to gb1AF067820 ATPase II from Homo sapiens

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LSIGDIVKVEKNEFPADVLVSSVEDAICVYETMNLGSLNKKVQGLVSSLRD  
ENFKGFEAFVKCEDPNANLYSFVGTMLKAGYPLSPQOLLRLRSLKLENTDFIGAV  
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DGMKRWYLRPDSSSIFDPKRAPVAAYIFLTAWMLYSIFIPISLYSIEIVKVLQS  
IFINQDIIHMYEADKPARARTSNLNEELQDVTILSDKTGTLICNSMEFICKSVAGT  
AYGRVTEVEMAGRRKGLPVQSDENDIMEYKEATEESTYKGFNFRDERINNG  
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FNRTOTTISRELDLVSGKRVERLYKVLNVLBNSTRKMSVIOVEDCKLLILCKGA  
DNVMERLSKNGREFEETRDHVNAYADAGLTLLIAYRELDEKEYKVNERNISEAKS  
SVSADRSLIEETEKDILILGATAVADKLQVPCIDKLAQAGKIWLVTGDK  
METAINIGFACSLLRQDMKQIINLEPEISLEKTEKDVIAKASKENVLQIINGK  
TOLKYSGGNALIIIDGSLAYALDDDIKHIFLELASVASCYICRSCSKQALVTRL  
VKSNGKTTLAIDGANDVQLQEAIDIGVIGSVEGMAVMSDIAIAQFYLRLRL  
VHGMCYRRISTMICYFFYKNITRGFTFLYETVYTTFSSTPAYNDWFLSYNVFESSL  
PVIALGVFDQDVSARYCLKFPILYQEGVQNVLFESRRILGWMPNGFYSAVIIFLCKS  
SLOSQAFNHDGKTPGREILGGTMYTCIVWVNLQMALAISYFTLIQHIWISVIVVY  
FFITYGELPSTRISTGAYKVFVEALAPLSYWLITLFFVVVATLMPFYIYSALQMSFPF

Query Match 21.5%; Score 105.6; DB 8; Length 98942;  
Best Local Similarity 58.5%; Pred. No. 8.8e-18;  
Matches 227; Conservative 0; Mismatches 149; Indels 12; Gaps 2;

QY 94 tgggtcaactggtcttgcactgtttttgatgaccctgcttaactgttttagttactagtgt 153  
Db 65547 TGGTCGACTGATTTGTGTAATGTTGGATGGACATAAATCATGCTGCTTGCATTGTTGG 65488

QY 154 tggccttgatcacctttggacagattctgaaataactaaacaaagaaacacttcagt 213  
Db 65487 TGCCCTTGTGTTGCCCTTGGACGATCGCGGAGGTGTAGACAGAGGTTCACATCGTGT 65428

QY 214 gggagtagaggtgcattatat-----tgttgctgggactgacagattgcctagc 264  
Db 65427 GGTGTGACGGGGGATGTACATGATCATATTGTTGACCGGGTATGAGGAGCAGT 65368

QY 265 ctatatctctctctacaggtctaaatgaggggccaatatgatctggaagaggcacct 324  
Db 65367 CTCTACTCTTCTGCTTTTACCAGCAACAACTTAGAGCCCAATACATACTCAAGGAGACCT 65308

QY 325 tgtgtgattgcttctgatactatctctgaaacctgtgcttcttgccagaatacaga 384  
Db 65307 TGTGTGACTGTTGTGTCCACTTTTGTGCGAGCCATGCGCCTCTTTGTCAGAGATATAGG 65248

QY 385 gagctt---aagaacctggcttcttgatgggaatagggtggcaagctaataatggataga 441  
Db 65247 CAACTTCAACACAAACCGGATTTGGACTTGGTCATCGGTTGGCATGGATATGGAACGA 65188

QY 442 caaagccggggagttaaccactgcacctt 469  
Db 65187 CATGCAGGACTTGTGCTCTACACCTT 65160

RESULT 8  
AF049928  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF049928 782 bp mRNA linear PLN 05-JUL-2000  
Petunia x hybrida PGPS/D12 (PGPS/D12) mRNA, complete cds.  
AF049928  
AF049928.1 GI:4105793  
Petunia x hybrida.  
Petunia x hybrida  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
1 (bases 1 to 782)  
Guyon,V.N., Astwood,J.D., Garner,E.C., Dunker,A.K. and Taylor,L.P.

**TITLE** Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia

**JOURNAL** Plant Physiol. 123 (2), 699-710 (2000)

**MEDLINE** 20317212

**PUBMED** 10859200

**REFERENCE** 2 (bases 1 to 782)

**AUTHORS** Guyon, V., Astwood, J.D. and Taylor, L.P.

**TITLE** Direct Submission

**JOURNAL** Submitted (23-FEB-1998) Genetics and Cell Biology, Washington State University, Science Hall, Pullman, WA 99164-4234, USA

**FEATURES** Location/Qualifiers

source 1..782

gene /organism="Petunia x hybrida"

CDs /db\_xref="taxon:4102"

kaempferol /tissue\_type="germinating petunia pollen treated with kaempferol"

1..782 /gene="PGPS/D12"

64..501 /gene="PGPS/D12"

/codon\_start=1

/product="PGPS/D12"

/protein\_id="A002554.1"

/db\_xref="GI:4105794"

/translation="MSDRPQVPMSSGICDFQDVKKCITCMPCITFGRIAEVADQG STCVVSGTVLYLVLTGFGCCWYSCFYRSKLNRQYILDEKPCSDLCTHCCEYCA LCOEYRELQNGQFDMSTGWNNENKMGSGALPPTVQAAMNR"

**BASE COUNT** 243 a 138 c 163 g 238 t

**ORIGIN**

Query Match 19.3%; Score 95; DB 8; Length 782;

Best Local Similarity 56.6%; Pred. No. 1.le-14;

Matches 201; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

Qy 94 tggccaactggtcttttgcactgttttgatgacccctgaacctgttagtttagttactagtgtt 153

Db 88 TGGCTCTCTGGTATATGTGATGCTCTCAAGATGTAAAGGCTGCTCTTAACATGTGG 147

Qy 154 tgcccttgatcaccttggacagattctgaaatactaaacaaaggaacaaacttcattgt 213

Db 148 TGCCCATGTATACATTTGGCCGATAGACAGAGTGCTGCTACCAAGATCCACTTCAATG 207

Qy 214 gggagtagaggtgcattatattgttctgggactgcagagatt-----gcctagc 264

Db 208 GTACTGAGTGGAAACAGTTTACCTATTGTTTATCTTGTGACGAGTGGGTTGGGTGTCG 267

Qy 265 ctatatcctgctctcacaggtctaaataggggggcaatatgactctggaagggcacct 324

Db 268 TGGTACTCGTGTCTTCTATCGTTCAAACTACGAAACCAATATTACTTTGGATGAAACCT 327

Qy 325 tgtttgatigtcttgatcatgtattctgtgaacctgtgctctcttgcgaagaatacaga 384

Db 328 TGCTCTGATCTCTGACCAATGTGTTGGAGTACTGCGCATTTGTCTCAAGAGTACAGA 387

Qy 385 gagcttaagacagctggctttgatggaatggatggggtggcaagctaataatggata 439

Db 388 GAGCTCCAGAACCAAGGCTTCGACATGTCCACAGAGTTTGGAAATGAAACATGGAAA 442

**RESULT** 9

**AP004003/c**

**LOCUS** AP004003 103550 bp DNA linear HTG 02-AUG-2001

**DEFINITION** Oryza sativa chromosome 2 clone OJ1124\_H01, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered pieces.

**ACCESSION** AP004003

**VERSION** AP004003.1 GI:15076811

**KEYWORDS** HTG; HTGS\_PHASE2.

**SOURCE** Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1124\_H01.

**ORGANISM** Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

**REFERENCE** 1 (bases 1 to 103550)

**AUTHORS** Sasaki, T., Matsumoto, T. and Yamamoto, K.

**TITLE** Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC clone:OJ1124\_H01

**JOURNAL** Published Only in Database (2001) In press

**REFERENCE** 2 (bases 1 to 103550)

**AUTHORS** Sasaki, T., Matsumoto, T. and Yamamoto, K.

**TITLE** Direct Submission

**JOURNAL** Submitted (01-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasakienas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

\* NOTE: This is a 'working draft' sequence.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and the accession number will be preserved.

**FEATURES** Location/Qualifiers

source 1..103550

/organism="Oryza sativa"

/cultivar="Nipponbare"

/db\_xref="taxon:4530"

/chromosome="2"

/clone="OJ1124\_H01"

**BASE COUNT** 29755 a 21927 c 21786 g 30082 t

**ORIGIN**

Query Match 18.5%; Score 90.8; DB 2; Length 103550;

Best Local Similarity 59.8%; Pred. No. 7.3e-14;

Matches 171; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

Qy 137 gtttagtactagtgttggccctgtatcaccttggacagattctgaaatacaca 196

Db 566 GTTTTATGACGTGGTGTGTGCCCGTCATCAGTTTCGGGACATCGCGAGATCGTCGACC 5607

Qy 197 aaggaacaaacttcatgtggagtagaggtgcattatattgttctgggactg---acag 253

Db 5606 GGGGGTCTGTCGTCTGCGGGACGACGGGTGCTGTGACGCTGCTTCCTCAGG 5547

Qy 254 gattgcctagcctatattcctgtcttctacaggtctcaaatgaggggcaatatgatctgg 313

Db 5546 GCTGCAGCTGTATCTACTCTCTGCATCTACCGTCCAAAGTCCGAGTACGGCCTGC 5487

Qy 314 aagaggcaacctgtgtgattgttctgttacaatgtattctgaaaccttgctcttttgc 373

Db 5486 AGGAGACGCCCTGCCCCGACTGCTCTCCACTTGTGTGGTGGAGCCCTGCGCCCTGCC 5427

Qy 374 aagaatacacagagcttaagaacctgtgcttctgtatgggaatagg 419

Db 5426 AGGAGTACCGCGAGCTCAGNAGCGCGCTTCGACATGAGCCTCGG 5381

**RESULT** 10

**AP004536**

**LOCUS** AP004536 78574 bp DNA linear PLN 14-DEC-2001

**DEFINITION** Lotus japonicus genomic DNA, chromosome 4, clone:Lj15N19, TM0097b, complete sequence.

**ACCESSION** AP004536

**VERSION** AP004536.1 GI:17736903

**KEYWORDS** HTG.

**SOURCE** Lotus japonicus DNA, clone:LjT library clone:Lj15N19.

**ORGANISM** Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)  
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

FEATURES  
    source  
        Location/Qualifiers  
            ..146017  
            /organism="Oryza sativa"  
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            /db\_xref="taxon:4530"  
            /chromosome="6"  
            /clone="P0528B02"  
BASE COUNT         41635 A 31780 C 31628 G 40874 T   100 others  
ORIGIN

Query Match                   15.1%; Score 74.2; DB 2; Length 146017;  
Best Local Similarity       59.9%; Pred. No. 1.7e-09;  
Matches 124; Conservative   0; Mismatches 83; Indels   0; Gaps   0;

QY   223 ggtgcattatattgcttggagactgacaggattgctagtcatattcgtctttac 282  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db   11757 GGACCTTGTATGTTTGCTGGCGACAATAAGGTGCCAATGGCTGTATGCTTGACAAA 11698  
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QY   283 agtgtcaaatgaggggacaatatgatctggaagacccttgattgattgttcgtta 342  
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db   11697 CGATCCTCAATGCGGCACAGTAACACTTCACACAGTCGCCCTCTGTGGACTGCTGGCGTC 11638  
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QY   343 catgtattctgtgaacctgtgctctttgccagaatacacagagcttaagaacctgtgc 402  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db   11637 CACTTCTTCGCATAGATTGTGGCTATGCCAAGATACAAAGGCTCGAAAAACGGCGC 11578  
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QY   403 ttigtatgggaatagggtggcaagct 429  
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Db   11577 TTCAACATGFCCAAAGGTCTTCTTGCT 11551  
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RESULT 12  
LOCUS AC006917/c  
DEFINITION Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence.  
ACCESSION AC006917  
VERSION AC006917.6 GI:4757662  
KEYWORDS HTG.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 132699)  
Chao,Q., Shinn,P., Dunn,P., Buehler,E., Kahn,S., Kim,C., Walker,M., Williams,S., Altafi,H., Araujo,R., Conn,L., Conway,A.B., Gonzalez,A., Hansen,N.F., Huizar,L., Kremenetskaia,I., Lenz,C., Li,J., Liu,S., Luros,S., Rowley,D., Schwartz,J., Toriumi,W., Vysotskaia,V., Yu,G., Davis,R.W., Federspiel,N.A., Theologis,A. and Ecker,J.R.  
Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I  
Unpublished  
2 (bases 1 to 132699)  
Ecker,J.R.  
Direct Submission  
Submitted (25-FEB-1999) Arabidopsis thaliana Genome Center,  
Department of Biology, University of Pennsylvania, 38th Street and  
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

```
REFERENCE
AUTHORS      3 (bases 1 to 132699)
TITLE        Ecker,J.R.
JOURNAL      Direct Submission
              Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center,
              Department of Biology, University of Pennsylvania, 38th Street and
              Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
REFERENCE
AUTHORS      4 (bases 1 to 132699)
              Cheuk,R., Shinn,P., Brooks,S., Buehler,E., Chao,Q.,
              Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,B., Chin,C.,
              Chlou,J., Choi,E., Conn,L., Conway,A., Gonzalez,A., Hansen,N.,
              Howling,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J.,
              Liu,S., Mukharsy,N., Nguyen,M., Palm,C., Pham,P., Sakano,H.,
              Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M.,
              Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J.
TITLE        Direct Submission
JOURNAL      Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
              Department of Biology, University of Pennsylvania, 38th and
              Hamilton Walk, Philadelphia, PA 19104-6018, USA
COMMENT      On May 7, 1999 this sequence version replaced gi:4731042.
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QY 304 tatgatctgaagagccacttggtgattgctgtgtacatgattctgtgaacctgtg 363
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RESULT 13
AB015477
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DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MOK9.
ACCESSION AB015477 BA000015
VERSION AB015477.1 GI:3241925
KEYWORDS Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
clone:MOK9.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (sites)
Nakamura,Y., Sato,S., Asamizu,E., Kaneko,T., Kotani,H., Miyajima,N.
and Tabata,S.
Submitted (17-JUN-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)

REFERENCE
AUTHORS Nakamura,Y.
TITLE Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen
physically assigned p1 and TAC clones
JOURNAL DNA Res. 5 (5), 297-308 (1998)
MEDLINE 99087489
REFERENCE 2 (bases 1 to 87459)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MOK9
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://combio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://greenlab.cba.ilstate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is K21B8 and the 3' clone is K2K18.

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ACCESSION AB026658 BA000014
VERSION AB026658.1 GI:4757414
KEYWORDS
SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui pl
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (sites)
Sato.S., Nakamura.Y., Kaneko.T., Katoh.T., Asamizu.E. and Tabata.S.
Structural analysis of Arabidopsis thaliana chromosome 3. I.
Sequence features of the regions of 4,504,864 bp covered by sixty
pl and TAC clones
DNA Res. 7 (2), 131-135 (2000)
20277480
JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 88989)
AUTHORS Sato.S., Nakamura.Y., Kaneko.T., Kato.T., Asamizu.E. and Tabata.S.
TITLE Direct Submission
```



## JOURNAL

Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)  
Address for correspondence: kaos@kazusa.or.jp  
For the latest information on annotation of this clone, please see <http://www.kazusa.or.jp/kaos/cgi-bin/aggd.graph.cgi?c=MYF24>  
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.  
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://gremmln1.zool.iastate.edu/cgi-bin/sp.cgi>).  
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MIE15 and the 3' clone is K24M9.

## FEATURES

## source

1. .88989  
Location/Qualifiers

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/chromosome="3"

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/clone="MYF24"

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similar to unknown protein"

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similar to unknown protein"



CDS  
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Qy 269 attctgtcttcacaggtctctaaatgaggggcaaatatgatctctggaagagggcacctttg 328  
Db 51508 ACTCATGTGATGTTCCGGGCCAAAATGCGAAACAAATACGGGTACCGGATGTCGGGCTC 51449  
Qy 329 ttgattgtctgtacatgtattctgtgaacctgtgtcttctcccaagaataacagagagc 388  
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Qy 389 ttaagaacccgtggcttgatgggaatagggtggcaagcgaatgatgat 438  
Db 51388 TCAAAACCGTGGTTTTCACCCCAATATGTTGAATTTATTTATTTATGAT 51339

RESULT 15  
EGU271639/c  
LOCUS EGU271639 469 bp DNA linear PLN 06-JAN-2001  
DEFINITION Elaeis guineensis microsatellite DNA, clone mEgCIR0230.  
ACCESSION AJ271639  
VERSION AJ271639.1 GI:12053789  
KEYWORDS microsatellite; repetitive DNA.  
SOURCE Elaeis guineensis.  
ORGANISM Elaeis guineensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Arecoidae;  
Coccolae; Elaeidinae; Elaeis.  
1 (bases 1 to 469)  
Billette,N., Risterucci,A.M., Barcelos,E., Amblard,P. and  
Bauriens,F.C.  
Development, characterization and across-taxa transferability of  
Elaeis guineensis SSR markers  
Unpublished

REFERENCE 2 (bases 1 to 469)  
AUTHORS Billette,N.  
TITLE Direct Submission  
JOURNAL Submitted (02-FEB-2000) Billette N., CP. Cirad, BP Avenue Agropolis  
F-34032 Montpellier CEDEX 1, 34032, FRANCE  
FEATURES  
Location/Qualifiers  
source  
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Best Local Similarity 60.3%; Pred. No. 3.5e-07;  
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Db 449 CATGTGGGACAGCTGGAGCGCTATATGTGATTCTTAAGGTCTTGACTAGGTGTCACATGGA 390  
Qy 266 tatattcctgtcttcacaggtctctaaatgaggggcaaatatgatctggaagagggcacctt 325  
Db 389 TATACTCGTGGTCTTTACAGATCCAAAGCTCAGATTGCAACTTGCCGGATTCCCTCTT 330  
Qy 326 gtgttgattgtctgtacatgtattctgtgaacctgtgtcttcttgcgaagaataacagag 385  
Db 329 GCTCGGACTGCTGTGTTCACATTTTCTCGGAGTGTGCTGGCCTTGTGTCAAGAGTATACAG 270  
Qy 386 agcttaagaacccgtggcttgatgggaatagg 419  
Db 269 AGCTCAGAAGCCGTGGATGATGATGACTATAGG 236  
Search completed: July 15, 2002, 08:28:45  
Job time: 6738 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:36:27 ; Search time 1598.68 Seconds  
(without alignments)  
4153.741 Million cell updates/sec

Title: US-09-898-659-1

Perfect score: 492

Sequence: 1 atgtatccaacggttaggata.....atgcaggcatgaccagggtga 492

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_gss.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165.6	33.7	610	10	BG459056
2	153	31.1	559	9	AI897534
3	153	31.1	585	9	AI778836
4	153	31.1	585	9	AW455311
5	153	31.1	633	9	AI778763
6	153	31.1	673	10	BI922710
7	153	31.1	719	9	AI778764
8	153	31.1	720	9	AI778837
9	151.4	30.8	544	9	AW040794
10	151.4	30.8	620	9	AI775220
11	151.4	30.8	624	9	AW092086
12	150.4	30.6	585	9	AW039653
13	149	30.3	711	10	BI922592
14	148.4	30.2	525	9	AI773903
15	147.6	30.0	415	10	BM176887
16	146.8	29.8	489	9	AW288052
17	146.8	29.8	568	10	BF519667

18	146.8	29.3	638	10	BI264661
19	146.8	29.3	645	10	BF646652
20	146.8	29.3	659	10	BG455061
21	146.8	29.3	683	10	BI263865
22	146.8	29.3	701	10	BG584553
23	146	29.7	499	10	BM177616
24	146	29.7	531	10	BM178944
25	146	29.7	555	10	BM143404
26	146	29.7	556	10	BM143488
27	146	29.7	556	10	BM177498
28	145	29.5	698	9	AW906026
29	144.4	29.3	491	10	BM187610
30	144.4	29.3	551	10	BM188361
31	144.4	29.3	565	10	BM188873
32	144.4	29.3	573	10	BM188528
33	143.8	29.2	566	10	BI123932
34	142.4	28.9	649	10	BG448256
35	141.2	28.7	543	9	AW781893
36	140.6	28.6	548	10	BI432374
37	140.2	28.5	555	9	AW756955
38	139.6	28.4	564	10	BE805908
39	139	28.3	506	10	BI434528
40	139	28.3	533	9	AI484746
41	138.4	28.1	698	10	BI433103
42	132.8	27.0	577	9	AJ407430
43	132.2	26.9	648	10	BF647753
44	131.6	26.7	515	10	BG510727
45	131.4	26.7	529	9	AI960277

## ALIGNMENTS

RESULT 1

BG459056

LOCUS

DEFINITION

ACCSSION

KEYWORDS

VERSION

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

BASE COUNT

ORIGIN

BG459056 610 bp mRNA linear EST 19-MAR-2001  
00829 leafy spurge Lambda HybrizAP 2.1 two-hybrid vector cDNA  
Library Euphorbia esula cDNA clone 35AE 5' similar to ORFX  
[Lycopersicon esculentum], accession# AAF74286, mRNA sequence.

BG459056  
BG459056.1 GI:13382381  
EST.  
leafy spurge.  
Euphorbia esula

Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.

Anderson, J.V. and Horvath, D.P.  
Identification of mRNAs expressed in underground adventitious buds  
of Euphorbia esula (leafy spurge)

Unpublished (2000)  
Contact: Anderson JV  
Plants Science Research

USDA/ARS, Biosciences Research Lab  
1605 Albrecht Blvd., PO Box 5674, Fargo, ND 58105, USA

Tel: 701 239 1263  
Fax: 701 239 1252  
Email: andersjv@fargo.ars.usda.gov

Seq primer: pAD5.  
Location/Qualifiers  
1. 610

/organism="Euphorbia esula"  
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/clone\_lib="leafy spurge Lambda HybrizAP 2.1 two-hybrid  
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/dev\_stage="3-day induced (decapitated)"

166 a 148 c 146 g 148 t 2 others

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Matches 256; Conservative 0; Mismatches 129; Indels 3; Gaps 1;

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Db 310 CETAAGCGGGGAGCAATATATGAGTACTAGCATGCTTTCACAGAGTATGGATGCTTATA 369
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QY 270 ttctcttctacagctcaaaatgaggggcaaatatctctggaagagggcacttctgt 329
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QY 330 tgattgtcttgcattgtattctgtgaaccttgtgctcttcttgcgaagaatacacagagct 389
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RESULT 2
AI897534
LOCUS EST266977 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLED27J18, mRNA sequence.
ACCESSION AI897534
VERSION AI897534.1 GI:5603436
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
          Lycopersicon.
REFERENCE 1 (bases 1 to 559)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
          Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
          ,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
          ,S.D. and Giovannoni,J.
          Generation of ESTs from tomato carpel tissue
          Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
          Location/Qualifiers
            1..559
              /organism="Lycopersicon esculentum"
              /cultivar="TA496"
              /db_xref="taxon:4081"
              /clone="cLED27J18"
              /clone_lib="tomato ovary, TAMU"
              /tissue_type="carpel"
              /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
              /lab_host="XL1-Blue MRF"
              /note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
              XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and
              directionally cloned cDNA in vector Lamda ZAP II with 5'

and 3' ends located at the EcoRI and XhoI sites,
respectively."
BASE COUNT 162 a 91 c 118 g 188 t
ORIGIN

Query Match      31.1%; Score 153; DB 9; Length 559;
Best Local Similarity 64.7%; Pred. No. 2e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

QY 94 tgggtcaactggctcttgcactgttttgatgacccctgtaactgttttagttactagtgt 153
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 150 TGGTCTACTGGGCTTTGTGATTGTTTCTCTGATATCTCGAGTTGTTGTTAACTTCTCTGG 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 154 tgcccttctacacctcttgacagatttctgaaataactaaacaaaggaacaaacttcagt 213
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 210 TGTCCATGATATACATTTTCGACAAATGCTGAAATTTGTCACAAAGGACAGTTTCTTGT 269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 214 gggagtagagggtgcattattgttctgtct---gggactgacaggattgcctagcctatat 270
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 270 GGTGCAAGTGGAGCTTTATATATTTTAAATAGAAGCATTAACAGGATGTGGATGATTTAT 329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 271 tctgtcttctacaggtctctaaatgaggggcaaatatgatactggaagagggcaccttgtgt 330
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 330 TCATGTTTTTATCGTACAAAATGAGAAAACAATACATGTTACCAAGAGCCCTTGTGG 389
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 331 gattgtctgtacatgtattctgtgaaccttgtgctcttcttgcgaagaatacacagagctt 390
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 390 GACTGTTGCTTCATTTTGTGTAATGTTGCTTTATGCCAAGAAACATCGTGACATC 449
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 391 aagaacctggtcttgatatgggaatagggtaggcaagctaatatgtagacaaagccg 450
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 450 AAACATCGTGGATATGACATGCTATTGTTGGCAAGGAAATATGATGATAACCAAAATGGA 509
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 451 ggagttaccatgcccc 467
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 510 GGAATAGCAATGGCTCC 526
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
AI778836
LOCUS EST259715 tomato susceptible, Cornell Lycopersicon esculentum cDNA
DEFINITION clone cLES6K8, mRNA sequence.
ACCESSION AI778836
VERSION AI778836.1 GI:5276877
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
          Lycopersicon.
REFERENCE 1 (bases 1 to 585)
AUTHORS D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
          Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
          ,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
          Giovannoni,J.J. and Martin,G.B.
          Generation of ESTs from Pseudomonas susceptible tomato
          Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
          Location/Qualifiers
            1..585
              /organism="Lycopersicon esculentum"
              /cultivar="R11-13 (Rio Grande x Money Maker)"
              /db_xref="taxon:4081"
              /clone="cLES6K8"
              /clone_lib="tomato susceptible, Cornell"

FEATURES
          source
            1..585
              /organism="Lycopersicon esculentum"
              /cultivar="R11-13 (Rio Grande x Money Maker)"
              /db_xref="taxon:4081"
              /clone="cLES6K8"
              /clone_lib="tomato susceptible, Cornell"
```

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/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLES - Tomato Pseudomonas Susceptible EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-)
) at 5' end with EcoRI and 3' end with XhoI site"
BASE COUNT 171 a 91 c 119 g 204 t
ORIGIN

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```

Query Match 31.1%; Score 153; DB 9; Length 585;
Best Local Similarity 64.7%; Pred. No. 2e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

QY 94 tggtaactggtcttctgaactgttttgatgacccctgtaactgttttagttactagtgtt 153
DB 148 TGGTCTACTGGGCTTTGTGATGTTCTCTGATATCTCGAGTTGTTGTTAACTTGCTGG 207

QY 154 tgccttgatcaccttgacagattctgaaatactaaacaaagaaacaaacttcagt 213
DB 208 TGTCCATGTTATACATTTGGCAAAATGCTGAAATTCGCACAAAGGAACAGTTCTTGT 267

QY 214 ggaagtagaggtgcattatattgttct---gggactgcagagattgacctagctatat 270
DB 268 GGTGCAAGTGGAGCTTTATATTTTAAATAGAAGCATTAACAGGATGTGGATGTTATTAT 327

QY 271 tctgtcttcacaggtctaaatagagggccaatatgactggaagagggcaccttgtgt 330
DB 328 TCATGTTTTTATCTACAAAAATGAGAAAAACAATACATGTTACCAAGAACCCCTTGTGGG 387

QY 331 gattgtcttgacatgtattctgtgaacctgtgctctttgccaagaatacacagagcctt 390
DB 388 GACTGTTTGTCTCATTTTGTGTGATGTTGCTTTATGCCAAGAACATCGTGAACCT 447

QY 391 aagaacgctggcttgataggaaggtggcaagctaatatggtatagacaaagccgg 450
DB 448 AACATCGTGGATGATGATGCTCTATTGTTGGCAAGGAATATGGATAACCAAAATGGA 507

QY 451 ggaattaccatgcccc 467
DB 508 GGAATAGCAATGGCTCC 524

```

```

RESULT 4
AW455311 585 bp mRNA linear EST 18-MAY-2001
LOCUS
DEFINITION
Lycopersicon esculentum cDNA clone cLEX10111 5', mRNA sequence.
ACCESSION
AW455311
VERSION
EST.
SOURCE
Lycopersicon
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1 (bases 1 to 585)
van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato root tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..585
/organism="Lycopersicon esculentum"

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```

/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEX10111"
/clone_lib="tomato root during/after fruit set, Cornell
University"
/tissue_type="root"
/dev_stage="plants during and after fruit-set"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
(USDA-ARS, Ithaca, NY 14850)."
BASE COUNT 171 a 91 c 119 g 204 t
ORIGIN

```

```

Query Match 31.1%; Score 153; DB 9; Length 585;
Best Local Similarity 64.7%; Pred. No. 2e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

QY 94 tggtaactggtcttctgaactgttttgatgacccctgtaactgttttagttactagtgtt 153
DB 148 TGGTCTACTGGGCTTTGTGATGTTCTCTGATATCTCGAGTTGTTGTTAACTTGCTGG 207

QY 154 tgccttgatcaccttgacagattctgaaatactaaacaaagaaacaaacttcagt 213
DB 208 TGTCCATGTTATACATTTGGCAAAATGCTGAAATTCGCACAAAGGAACAGTTCTTGT 267

QY 214 ggaagtagaggtgcattatattgttct---gggactgcagagattgacctagctatat 270
DB 268 GGTGCAAGTGGAGCTTTATATTTTAAATAGAAGCATTAACAGGATGTGGATGTTATTAT 327

QY 271 tctgtcttcacaggtctaaatagagggccaatatgactggaagagggcaccttgtgt 330
DB 328 TCATGTTTTTATCTACAAAAATGAGAAAAACAATACATGTTACCAAGAACCCCTTGTGGG 387

QY 331 gattgtcttgacatgtattctgtgaacctgtgctctttgccaagaatacacagagcctt 390
DB 388 GACTGTTTGTCTCATTTTGTGTGATGTTGCTTTATGCCAAGAACATCGTGAACCT 447

QY 391 aagaacgctggcttgataggaaggtggcaagctaatatggtatagacaaagccgg 450
DB 448 AACATCGTGGATGATGATGCTCTATTGTTGGCAAGGAATATGGATAACCAAAATGGA 507

QY 451 ggaattaccatgcccc 467
DB 508 GGAATAGCAATGGCTCC 524

```

```

RESULT 5
AW1778763 633 bp mRNA linear EST 18-MAY-2001
LOCUS
DEFINITION
EST259642 tomato susceptible, Cornell Lycopersicon esculentum cDNA
clone cLES6C20, mRNA sequence.
ACCESSION
AW1778763
VERSION
EST.
SOURCE
tomato.
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1 (bases 1 to 633)
D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas susceptible tomato
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html

```

```

5 prime sequence.
FEATURES             Location/Qualifiers
  source              1..633
    /organism="Lycopersicon esculentum"
    /cultivar="Ril-13 (Rio Grande x Money Maker)"
    /db_xref="taxon:4081"
    /clone="cLES6C20"
    /clone_lib="tomato susceptible, Cornell"
    /tissue_type="leaf"
    /dev_stage="4-week old"
    /lab_host="SOLr"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLES - tomato Pseudomonas Susceptible EST Library.
Directionally cloned cDNAs inserted into pBluescript SK(-)
) at 5' end with EcoRI and 3' end with XhoI site"
BASE COUNT          189 a 91 c 128 g 225 t
ORIGIN
1
Query Match          31.1%; Score 153; DB 9; Length 633;
Best Local Similarity 64.7%; Pred. No. 2.1e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;
QY 94 tggtaactggtttgtcactgttttgatgaccctgctaactgttttagtactagtgtt 153
Db 148 TGTCTACTGGGCTTTGTGATTTCTCTGATATCTCGAGTTGTGTTAACTTGCTGG 207
QY 154 tgccttgatcacctttggacagattctgaaataactaaagaaacacattcatgt 213
Db 208 TGTCCATGTATTACATTTGGCAAAATGCTGAAATGTGCAAGACAGATTTCTTGT 267
QY 214 gggagttagggtgcattattgtttgct---gggactgacaggattgcttagcctat 270
Db 268 GGTGCAAGTGGAGCTTTATATTTTAAATAGAAGCATTAACAGGATGTGGATTTAT 327
QY 271 tctgctttacaggtctaaaatgaggggcaatatgatctggaaagagcaccttgtt 330
Db 328 TCATGTTTTATCGTACAAAATGAGAAAACAATACATGTTACCAAGAAAGCCCTTGGG 387
QY 331 gattgtctgtacatgtattctgtgacacctgtgctcttggcaagaatacacagagctt 390
Db 388 GACTGTTGCTTCATTTTCTGTGATGTGTGCTTTATGCAAGAAACATCGTGAACTC 447
QY 391 aagaacccgtgcttgatgggaataggggtggcaagctaatatgatgatgacaaagccgg 450
Db 448 AAACATCGTGGATAGACATGTCTATTGTTGGCAAGGAAATATGGATAACCAAAATGGA 507
QY 451 gaggattaccatgccccc 467
Db 508 GGAATAGCAATGGCTCC 524

RESULT 6
BI922710 673 bp mRNA linear EST 18-OCT-2001
LOCUS EST542614 tomato callus Lycopersicon esculentum cDNA clone
DEFINITION cLEC78G14 5' end, mRNA sequence.
ACCESSION BI922710
VERSION BI922710.1 GI:16220768
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 673)
AUTHORS Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin
,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
FEATURES             Location/Qualifiers
  source              1..673
    /organism="Lycopersicon esculentum"
    /cultivar="TA496"
    /db_xref="taxon:4081"
    /clone="cLEC78G14"
    /clone_lib="tomato callus"
    /tissue_type="callus"
    /dev_stage="25-40 days old"
    /lab_host="XLI-Blue MRF"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLEC - Cotyledons Of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
BASE COUNT          201 a 91 c 138 g 243 t
ORIGIN
1
Query Match          31.1%; Score 153; DB 10; Length 673;
Best Local Similarity 64.7%; Pred. No. 2.1e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;
QY 94 tggtaactggtttgtcactgttttgatgaccctgctaactgttttagtactagtgtt 153
Db 148 TGTCTACTGGGCTTTGTGATTTCTCTGATATCTCGAGTTGTGTTAACTTGCTGG 207
QY 154 tgccttgatcacctttggacagattctgaaataactaaagaaacacattcatgt 213
Db 208 TGTCCATGTATTACATTTGGCAAAATGCTGAAATGTGCAAGACAGATTTCTTGT 267
QY 214 gggagttagggtgcattattgtttgct---gggactgacaggattgcttagcctat 270
Db 268 GGTGCAAGTGGAGCTTTATATTTTAAATAGAAGCATTAACAGGATGTGGATTTAT 327
QY 271 tctgctttacaggtctaaaatgaggggcaatatgatctggaaagagcaccttgtt 330
Db 328 TCATGTTTTATCGTACAAAATGAGAAAACAATACATGTTACCAAGAAAGCCCTTGGG 387
QY 331 gattgtctgtacatgtattctgtgacacctgtgctcttggcaagaatacacagagctt 390
Db 388 GACTGTTGCTTCATTTTCTGTGATGTGTGCTTTATGCAAGAAACATCGTGAACTC 447
QY 391 aagaacccgtgcttgatgggaataggggtggcaagctaatatgatgatgacaaagccgg 450
Db 448 AAACATCGTGGATAGACATGTCTATTGTTGGCAAGGAAATATGGATAACCAAAATGGA 507
QY 451 gaggattaccatgccccc 467
Db 508 GGAATAGCAATGGCTCC 524

RESULT 7
BI922764 719 bp mRNA linear EST 18-MAY-2001
LOCUS EST259643 tomato susceptible, Cornell Lycopersicon esculentum cDNA
DEFINITION clone cLES6C20, mRNA sequence.
ACCESSION BI922764
VERSION BI922764.1 GI:5276805
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

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Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 719)
D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman
, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas susceptible tomato
Unpublished (1999)
Contact: CUCI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES             Location/Qualifiers
   source             1..719
                     /organism="Lycopersicon esculentum"
                     /cultivar="R11-13 (Rio Grande x Money Maker)"
                     /db_xref="taxon:4081"
                     /clone="cLES6C20"
                     /clone_lib="tomato susceptible, Cornell"
                     /tissue_type="leaf"
                     /dev_stage="4-week old"
                     /lab_host="SOLR"
                     /note="vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
                     xhoI; cLES - Tomato Pseudomonas Susceptible EST library.
                     Directionally cloned cDNAs inserted into pBlueScript SK(-)
                     ) at 5' end with EcoRI and 3' end with xhoI site"

BASE COUNT          213 a   93 c  153 g   260 t
ORIGIN
Query Match          31.1%; Score 153; DB 9; Length 719;
Best Local Similarity 64.7%; Pred. No. 2.2e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

Qy  94  tggtaactggtctttgtcactggttttgatgacctgtctaactgttttagttactagtgtt 153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  148  TGGTCTACTGGGCTTTGTGATTGTTTCTCTGATATCTCGAGTTTCTGTTAACTTGCTGG 207

Qy  154  tgccttgtatcaccttggacagattctgaaatactaaacaagaagaacaacttcattgt 213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  208  TGTCCATGTATTACATTTGGACAAATTCGTAATTCGACAAAGGAACAGTTTCTTGT 267

Qy  214  gggagtagaggtgattattgttctgtct---gggactgacagattgcctagcctatat 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  268  GGTCAAGTGGAGCTTTATATTTTAAAGAACATTACAGGATGTGGATGATTATTAT 327

Qy  271  tcctgctctacaggtctaaatgaggggccaatatgatctctggaagaggccacttctgtt 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  328  TCATGTTTTTATCTACAAAAATCAGAAAAACAATACATGTTACCAAGAAAGCCCTTGTGGG 387

Qy  331  gattgcttgtacatgtattctgtgaaccttgcctcttggccaaataacagagagctt 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  388  GACTGTTTGTCTTCAATTTTGTGTAATGTGCTTTATGCCAAGAACATCGTGAAC 447

Qy  391  aagaacccgtgcttgcataatggaataggggtgccaagctaataatggtatagacaagccgg 450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  448  AAACATCTGGATATGACATGCTATTGGTTGGCAGGAATATGGATACCAAAATGGA 507

Qy  451  ggagttaccatgcccc 467
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  508  GGAATAGCAATGGCTCC 524

RESULT 8
AI1778837
LOCUS EST259716 tomato susceptible, Cornell Lycopersicon esculentum cDNA
DEFINITION clone cLES6K8, mRNA sequence.
ACCESSION AI1778837
VERSION AI1778837.1 GI:5276878

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KEYWORDS EST.
SOURCE Lycopersicon esculentum tomato.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 720)
D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman
, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas susceptible tomato
Unpublished (1999)
Contact: CUCI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES             Location/Qualifiers
   source             1..720
                     /organism="Lycopersicon esculentum"
                     /cultivar="R11-13 (Rio Grande x Money Maker)"
                     /db_xref="taxon:4081"
                     /clone="cLES6K8"
                     /clone_lib="tomato susceptible, Cornell"
                     /tissue_type="leaf"
                     /dev_stage="4-week old"
                     /lab_host="SOLR"
                     /note="vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
                     xhoI; cLES - Tomato Pseudomonas Susceptible EST library.
                     Directionally cloned cDNAs inserted into pBlueScript SK(-)
                     ) at 5' end with EcoRI and 3' end with xhoI site"

BASE COUNT          213 a   93 c  153 g   260 t   1 others
ORIGIN
Query Match          31.1%; Score 153; DB 9; Length 720;
Best Local Similarity 64.7%; Pred. No. 2.2e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

Qy  94  tggtaactggtctttgtcactggttttgatgacctgtctaactgttttagttactagtgtt 153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  148  TGGTCTACTGGGCTTTGTGATTGTTTCTCTGATATCTCGAGTTTCTGTTAACTTGCTGG 207

Qy  154  tgccttgtatcaccttggacagattctgaaatactaaacaagaagaacaacttcattgt 213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  208  TGTCCATGTATTACATTTGGACAAATTCGTAATTCGACAAAGGAACAGTTTCTTGT 267

Qy  214  gggagtagaggtgattattgttctgtct---gggactgacagattgcctagcctatat 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  268  GGTCAAGTGGAGCTTTATATTTTAAAGAACATTACAGGATGTGGATGATTATTAT 327

Qy  271  tcctgctctacaggtctaaatgaggggccaatatgatctctggaagaggccacttctgtt 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  328  TCATGTTTTTATCTACAAAAATCAGAAAAACAATACATGTTACCAAGAAAGCCCTTGTGGG 387

Qy  331  gattgcttgtacatgtattctgtgaaccttgcctcttggccaaataacagagagctt 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  388  GACTGTTTGTCTTCAATTTTGTGTAATGTGCTTTATGCCAAGAACATCGTGAAC 447

Qy  391  aagaacccgtgcttgcataatggaataggggtgccaagctaataatggtatagacaagccgg 450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  448  AAACATCTGGATATGACATGCTATTGGTTGGCAGGAATATGGATACCAAAATGGA 507

Qy  451  ggagttaccatgcccc 467
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  508  GGAATAGCAATGGCTCC 524

RESULT 9
AW040794

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LOCUS AW040794 544 bp mRNA linear EST 18-MAY-2001  
 DEFINITION EST283658 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA  
 clone cLE10H19, mRNA sequence.  
 ACCESSION AW040794  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 544)  
 D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,  
 Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,  
 Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni  
 J.  
 TITLE Generation of ESTs from tomato leaf tissue  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.  
 FEATURES  
 Location/Qualifiers  
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 /organism="Lycopersicon esculentum"  
 /cultivar="Rio Grande PtoR"  
 /db\_xref="taxon:4081"  
 /clone="cLE10H19"  
 /clone\_lib="tomato mixed elicitor, BTI"  
 /tissue.type="leaf"  
 /dev\_stage="4-6 week old plants"  
 /lab\_host="XLL-Blue MRF,"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; cLE1 - Inoculated with a variety of disease response  
 elicitors. Plants exposed to 2,6 dichloroisonicotinic  
 acid, BTH, jasmonic acid, ethylene, fenthion, EIX,  
 okadaic acid, or systemin prior to tissue harvest. EcoRI  
 site was destroyed during cloning."  
 BASE COUNT 154 a 90 c 117 g 183 t  
 ORIGIN  
 Query Match 30.8%; Score 151.4; DB 9; Length 544;  
 Best Local Similarity 64.5%; Pred. No. 6e-35;  
 Matches 243; Conservative 0; Mismatches 131; Indels 3; Gaps 1;  
 QY 94 tggtaactggttttgcactgttttgatgacctgctaactgttttagttagttagt 153  
 DB 148 TGGTCTACTGGGCTTTGCTGATTTCTCTGATATCTCGAGTTGTTGTTAACTTCTGG 207  
 QY 154 tgccttgatcacctttggacagattctgaaataactaaacaaagaaacactcatgt 213  
 DB 208 TGTCATGATATTACATTTGGACAAATGCTGAAATGTCGACAAAGAACAGTTTCTTGT 267  
 QY 214 gggagtagaggtgcattattgttggct---gggactgacaggttgccctgacctat 270  
 DB 268 GGTGCAAGTGGACCTTATATTTTAAATAGAAGCATTAACAGGATGTGGATGATTTAT 327  
 QY 271 tctgtcttacaggtctataaagtgggggcaataatgactctggaagaggcaacctgtgtt 330  
 DB 328 TCATGTTTTTATCGTACAAAAATGAGAAAAACAATACATGTTACACAGAAAGCCCTTGGG 387  
 QY 331 gattgtcttgacatattctgtgacctgtgtctcttggcaagaataacagagagctt 390  
 DB 388 GACTGTGCTTCATTTTGTGTGAATGTTGTGCTTTATGTCACAGAAATCGTGAACATC 447  
 QY 391 aagaacccgtggtttgatattggaaatagggtggcaagctaaatgtagtagacaagccgg 450  
 DB 448 AAACATCGTGGATGCACATGCTATTGTTGGCAAGGAAATATGATACCAACCAATGGA 507

QY 451 ggagttaccatgcccc 467  
 DB 508 GGGATAGCAATGGCTCC 524  
 RESULT 10  
 LOCUS AI775220 620 bp mRNA linear EST 18-MAY-2001  
 DEFINITION EST256320 tomato resistant, Cornell Lycopersicon esculentum cDNA  
 clone cLER14L22, mRNA sequence.  
 ACCESSION AI775220  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 620)  
 D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,  
 Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman  
 C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,  
 Giovannoni,J.J. and Martin,G.B.  
 TITLE Generation of ESTs from Pseudomonas resistant tomato  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.  
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 Location/Qualifiers  
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 /organism="Lycopersicon esculentum"  
 /cultivar="Kil-12 (35S):Pto in Rio Grande x Money Maker)"  
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 /clone="cLER14L22"  
 /clone\_lib="tomato resistant, Cornell"  
 /tissue.type="leaf"  
 /dev\_stage="4-week old"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; cLER - Tomato Pseudomonas Resistant EST Library.  
 Directionally cloned cDNAs inserted into pBluescript SK(-  
 ) at 5' end with EcoRI and 3' end with XhoI site."  
 BASE COUNT 184 a 85 c 135 g 215 t  
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 Query Match 30.8%; Score 151.4; DB 9; Length 620;  
 Best Local Similarity 64.5%; Pred. No. 6.3e-35;  
 Matches 243; Conservative 0; Mismatches 131; Indels 3; Gaps 1;  
 QY 94 tggtaactggttttgcactgttttgatgacctgctaactgttttagttagttagt 153  
 DB 102 TGGTCTACTGGGCTTTGCTGATTTCTCTGATATCTCGAGTTGTTGTTAACTTCTGG 161  
 QY 154 tgccttgatcacctttggacagattctgaaataactaaacaaagaaacactcatgt 213  
 DB 162 TGTCATGATATTACATTTGGACAAATGCTGAAATGTCGACAAAGAACAGTTTCTTGT 221  
 QY 214 gggagtagaggtgcattattgttggct---gggactgacaggttgccctgacctat 270  
 DB 222 GGTGCAAGTGGACCTTATATTTTAAATAGAAGCATTAACAGGATGTGGATGATTTAT 281  
 QY 271 tctgtcttacaggtctataaagtgggggcaataatgactctggaagaggcaacctgtgtt 330  
 DB 282 TCATGTTTTTATCGTACAAAAATGAGAAAAACAATACATGTTACACAGAAAGCCCTTGGG 341  
 QY 331 gattgtcttgacatattctgtgacctgtgtctcttggcaagaataacagagagctt 390  
 DB 342 GACTGTGCTTCATTTTGTGTGAATGTTGTGCTTTATGTCACAGAAATCGTGAACATC 401







BASE COUNT 146 a 90 c 109 g 180 t  
ORIGIN  
Query Match 30.2%; Score 148.4; DB 9; Length 525;  
Best Local Similarity 64.2%; Pred. No. 4.8e-34;  
Matches 240; Conservative 0; Mismatches 131; Indels 3; Gaps 1;  
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Db 148 TGGTCTACTGGCTTGTGATGTTCTCTGATATCTCGAGTTGCTGTTAACTTGCCTGG 207  
Qy 154 tgccttctacacacttggagagattctctgaataactaaacaaaggacaacttcgt 213  
Db 208 TGTCCATGTATTACATTTGGCAAAATGCTGAAATGTCGACAAAGGAACAGTTCTTGT 267  
Qy 214 gggagtagagtgcaattattttgtgt---ggagctgacagagatttcctagcctat 270  
Db 268 GTGCAAGTGGAGCTTTATATATTTTAAAGACATTAACAGGATGCGATGTTATTAT 327  
Qy 271 tctgtctctacagctcaaaatgagggggcaaatatcatctggaaggagcaccttgtgt 330  
Db 328 TCATGTTTTATCGTACAAAATGAGAAACAATACATGTTACCGAAGGCCCTTGTGGG 387  
Qy 331 gattcctctgtacatgtattctgtgaacctgtgtctcttggccaaagaatacagagctt 390  
Db 388 GACTGTTTGTCTCATTTTGTGTGTAATGTTGTGCTTATGCGCAAGAACATCGTGAAC 447  
Qy 391 aagaacctggcttgataggaataggggaagtggaagtaatatagatagacaaagccgg 450  
Db 448 AAACATCGTGGATATGACATGCTATTGTTGGCAAGGAAATATATGGAACCAAAATGGA 507  
Qy 451 ggagttaccatgcc 464  
Db 508 GGGATAGCAATGGC 521

RESULT 15  
BM176887  
LOCUS  
DEFINITION saj74805.y1 Gm-cl074 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl074-2313 5' similar to TR:Q9SX24 Q9SX24 F24J5.15 PROTEIN. ; , mRNA linear EST 06-DEC-2001  
ACCESSION BM176887  
VERSION BM176887  
KEYWORDS EST.  
SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpeliding,J., Coryell,V., Khanna,A., Bolla,B., Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
JOURNAL  
COMMENT Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com

Trace considered overall poor quality  
Seq primer: -40Rp from Gibco  
High quality sequence stop: 1.  
FEATURES  
Location/Qualifiers  
Source  
1..415  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
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/clone\_lib="Gm-cl074"  
/tissue\_type="seedlings induced for HR (hypersensitive response)"  
/dev\_stage="9-11 day old"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2: XhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR (hypersensitive response) by vacuum infiltrating plant tissue with Pseudomonas syringae pv. glycinea carrying the avrB gene (Genetics 141:1597-1604). Plant tissue (expanded unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)." 89 a 92 c 114 g 120 t  
BASE COUNT  
ORIGIN  
Query Match 30.0%; Score 147.6; DB 10; Length 415;  
Best Local Similarity 63.8%; Pred. No. 7.7e-34;  
Matches 241; Conservative 0; Mismatches 134; Indels 3; Gaps 1;  
Qy 94 tggtaactggtcttctgcaactgttttgatgaccctgctaactgttttagtactagtgtt 153  
Db 2 TGGTCCACCGCCTCTGTGACTGCTTCTCCGAATGCGAAACTGTTGCATGACGTTGG 61  
Qy 154 tgccttctacacacttggagagattctctgaataactaaacaaaggacaacttcagt 213  
Db 62 TGTCCATGTATTACCTTTGGCCGAGTTGACAGAAATGTTGACAGGGATCCACATCATGT 121  
Qy 214 gggagtagagtgcaattattttgtgt---gggagctgacagagatttcctagcctat 270  
Db 122 GGTGCTAGTGGGGCTCTGTATACCTTTATTTGCTGAGTCATTTGGCTGTGGCTATAC 181  
Qy 271 tctgtctctacagctctaaatgagggggcaatatcatctgtggaagagcacttggtt 330  
Db 182 TCTTGCTTCTACCGCCCAAGATGAGACGACAGTAGTATGCTCTAAAGGGAATGTTGTTCCG 241  
Qy 331 gattgtcttgtacatgtattctgtgaacctgtgtctcttcccaagaatacagaagctt 390  
Db 242 GATTGCTTGAATCAATGTTGTTTGGAGCCCTGCGCCCTCTGTCAAGAATATATCGTAGCT 301  
Qy 391 aagaacctggcttcttgatagggaatagggtggcaagctaataatgatatagacaaagccgg 450  
Db 302 CAACACCGTGGATTTCATGATGATTTATTTGGTGGGATGGAATATGTCGACAGCAAGACTCG 361  
Qy 451 ggagttaccatgccct 468  
Db 362 GGAGTAGCCATGACTGCT 379

Search completed: July 15, 2002, 07:56:22  
Job time: 4795 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 07:56:27 ; Search time 177.53 seconds  
(without alignments)  
4758.192 Million cell updates/sec

Title: US-09-898-659-1  
Perfect score: 492  
Sequence: 1 atgtatcaacggttagata.....atgcagcgatgaccaggatga 492

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	123.6	25.1	459	21 AAC46096	Arabidopsis thalia
2	123.6	25.1	523	21 AAC45096	Arabidopsis thalia
3	114	23.2	456	21 AAC46412	Arabidopsis thalia
4	105.6	21.5	675	21 AAC37426	Arabidopsis thalia
5	80.2	16.3	673	21 AAC35065	Arabidopsis thalia
6	78.6	16.0	692	19 AAV66762	Pathogen response
7	60.4	12.3	1044	21 AAC45640	Arabidopsis thalia
8	60.4	12.3	1046	21 AAC33819	Arabidopsis thalia
9	53.4	10.9	292	21 AAC32768	Arabidopsis thalia

0	51.4	10.4	749	21 AAC48702	Arabidopsis thalia
1	51.4	10.4	793	21 AAC36679	Arabidopsis thalia
2	47	9.6	958	21 AAC35015	Arabidopsis thalia
3	45.4	9.2	953	21 AAC50407	Arabidopsis thalia
4	40.6	8.3	1897	21 AAC49629	Arabidopsis thalia
5	40.6	8.3	1898	21 AAC36743	Arabidopsis thalia
6	39.6	8.0	1341	18 AAV74759	Staphylococcus aur
7	34.2	7.0	429	21 AAC04289	Human secreted pro
8	34.2	7.0	34980	22 AAH68527	C glutamylcudin
9	33.8	6.9	7607	14 AAQ49754	pTK gene LpTK-2.
10	33.8	6.9	7607	16 AAQ703097	Protein tyrosine-k
11	33.6	6.8	479	21 AA43011	Human 5' EST isola
12	33.6	6.8	602	20 AA208840	Gene No. 30 encodi
13	33.6	6.8	697	22 AAH68584	Human protein HP10
14	33.6	6.8	703	20 AA40821	Secreted protein E
15	33.6	6.8	795	21 AA564336	Clone 2790708 of a
16	33.6	6.8	795	21 AA562750	cDNA sequence #537
17	33.6	6.8	864	21 AAC76775	Human ORFX ORF2330
18	33.6	6.8	891	21 AAC98118	Human colon cancer
19	33.6	6.8	1183	22 AAH6728	Human polynucleoti
20	33.2	6.7	829	21 AAC34836	Arabidopsis thalia
21	33.2	6.7	3222	19 AAX14584	H. pylori GHPO 167
22	32.8	6.7	477	22 ABA46196	Human breast cell
23	32.8	6.7	477	22 ABA26363	Probe #4829 for ge
24	32.8	6.7	477	22 AAI36348	Probe #5034 used t
25	32.8	6.7	6407	24 ABL32943	Human immune syste
26	32.6	6.6	3006	21 AAA61054	Asparagus asparagi
27	32.2	6.5	761	20 AAZ33842	Tobacco plant resi
28	32	6.5	762	20 AAZ17581	Human gene express
29	32	6.5	3254	22 AAH29739	S cerevisiae apopt
30	32	6.5	6255	24 ABL32960	Human immune syste
31	32	6.5	611590	21 AAF22303	Arabidopsis thalia
32	31.8	6.5	23815	22 AAK68678	Human immune/haema
33	31.8	6.5	23815	22 AAK85169	Human immune/haema
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ALIGNMENTS

TT 1096  
AAC46096 standard; DNA; 459 BP.

AAC46096;

18-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 48995.

Hybridisation assay; genetic mapping; gene expression control;  
protein identification; signal transduction pathway;  
metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-01281825.  
05-MAR-1999; 99US-0123180.  
09-MAR-1999; 99US-0123548.  
23-MAR-1999; 99US-0125788.  
25-MAR-1999; 99US-0126264.  
29-MAR-1999; 99US-0126785.  
01-APR-1999; 99US-0127462.  
06-APR-1999; 99US-0128234.  
08-APR-1999; 99US-0128714.  
16-APR-1999; 99US-0129845.

ALIGNMENTS

RESULT 1  
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ID AAC46096 standard; DNA; 459 BP.  
XX  
AC AAC46096;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48895.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 390US-0121825.  
PR 05-MAR-1999; 390US-0123180.  
PR 09-MAR-1999; 390US-0123548.  
PR 23-MAR-1999; 390US-0125788.  
PR 25-MAR-1999; 390US-0126264.  
PR 29-MAR-1999; 390US-0126785.  
PR 01-APR-1999; 390US-0127462.  
PR 06-APR-1999; 390US-0128234.  
PR 08-APR-1999; 390US-0128714.  
PR 16-APR-1999; 390US-0129845.

PR	19-APR-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
PR	21-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
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KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
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XX	06-SEP-2000.
XX	25-FEB-2000; 2000EP-0301439.
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
XX metabolic pathway; promoter; termination sequence; ss.

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DT 17-OCT-2000 (first entry)
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KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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OW nucleic - nucleic search, using sw model

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.8	6.9	2770	4	US-08-426-509A-5
2	33.8	6.9	2770	5	PCT-US95-05008-5
3	33.8	6.9	7607	1	US-08-222-616-19
4	33.8	6.9	7607	5	PCT-US95-04228-19
5	33.6	6.8	703	4	US-09-247-155-79
6	32.6	6.6	7218	1	US-08-232-463-14
7	31.6	6.4	731	4	US-08-998-416-254
8	31.6	6.4	3907	3	US-08-475-742-1
9	31.4	6.4	5261	1	US-08-045-806-3
10	31.4	6.4	5261	1	US-08-366-051B-3
11	30.6	6.2	1607	1	US-08-446-908-1
12	30.6	6.2	1607	1	US-08-231-205A-1
13	30.6	6.2	1607	2	US-08-871-161-1
14	30.6	6.2	7917	2	US-08-167-854-1
15	30.4	6.2	7218	1	US-08-232-463-14
16	29.2	5.9	6840	4	US-08-980-241-8
17	29	5.9	1785	4	US-09-377-155-8
18	29	5.9	1785	4	US-09-669-974-8
19	28.6	5.8	383	1	US-08-620-467A-10
20	28.6	5.8	383	1	US-08-348-572-10
21	28.6	5.8	383	3	US-09-041-090B-10
22	28.4	5.8	1697	1	US-08-472-028A-9
23	28.4	5.8	1697	4	US-09-071-296-9
24	28.4	5.8	1697	4	US-09-196-268-9
25	28.4	5.8	1697	4	US-09-015-683-9
26	28.4	5.8	1697	4	US-09-191-998-9
27	28.2	5.7	552	2	US-08-078-311-18

28	28.2	5.7	552	2	US-08-460-402-18	Sequence 18, Appl
29	28.2	5.7	1216	2	US-08-078-311-20	Sequence 20, Appl
30	28.2	5.7	1216	2	US-08-460-402-20	Sequence 20, Appl
31	28.2	5.7	1307	2	US-08-078-311-17	Sequence 17, Appl
32	28.2	5.7	1307	2	US-08-460-402-17	Sequence 17, Appl
c 33	28.2	5.7	1623	1	US-08-121-202-3	Sequence 3, Appl
c 34	28.2	5.7	1644	4	US-08-821-994-71	Sequence 71, Appl
35	28.2	5.7	2046	1	US-08-184-327A-1	Sequence 1, Appl
36	28.2	5.7	2046	5	PCT-US95-00670-1	Sequence 1, Appl
c 37	28.2	5.7	4334	2	US-08-670-707A-38	Sequence 38, Appl
c 38	28.2	5.7	4334	4	US-09-037-601-38	Sequence 38, Appl
c 39	28.2	5.7	6402	2	US-08-670-707A-36	Sequence 36, Appl
c 40	28.2	5.7	6402	4	US-09-037-601-36	Sequence 36, Appl
41	28	5.7	3846	2	US-08-845-161A-5	Sequence 5, Appl
42	28	5.7	3846	4	US-09-270-751-5	Sequence 5, Appl
c 43	27.8	5.7	7493	1	US-08-212-133A-7	Sequence 7, Appl
c 44	27.8	5.7	7493	1	US-08-474-503-5	Sequence 5, Appl
c 45	27.8	5.7	7493	2	US-08-670-707A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-08-426-509A-5  
; Sequence 5, Application US/08426509A  
; Patent No. 6326469  
; GENERAL INFORMATION:  
; APPLICANT: Ullrich,, Axel  
; APPLICANT: Gishizsky,, Mikhail  
; APPLICANT: Sures,, Irman G.  
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN  
; TITLE OF INVENTION: TYROSINE KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York,  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/426,509A  
; FILING DATE: 21-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/232,545  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi,, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-0074-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2770 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
US-08-426-509A-5

Query Match 6.9%; Score 33.8; DB 4; Length 2770;  
Best Local Similarity 49.2%; Pred. No. 0.14;  
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;





	Query Match	6.6%	Score 32.6;	DB 1;	Length 7218;
	Best Local Similarity	6.6%;	Pred. No. 0.57;		
	Matches	20;	Conservative 153;	Mismatches 132;	Indels 0; Gaps 0;
QY	184	gaatactaacaagaacaaacttcattgtgggagtagaggcgatcatattgtttctgtc	243		
		: :			
Db	1337	RRR	1278		
QY	244	ggactgcagagtgcctagcctatatctctgtctcacaggctcaaatgaggggccaa	303		
		: :			
Db	1277	RRR	1218		
QY	304	tatgatctgaagaggccaccttgctgattgtcttgcacatgtattctgtgaaccttgt	363		
		: :			
Db	1217	RRR	1158		
QY	364	gctcttgccaagaatacacagagcttaagaaccgtgcttgcataTggaataaggctg	423		
		: :			
Db	1157	RRR	1098		
QY	424	caagctaatatggatagacaaaagccggggagttaccatgcccccattcatcaggcgatg	483		
		: : : : : : : : : : : : : : : :			



RESULT 8  
US-08-475-742-1  
; Sequence 1, Application US/08475742  
; Patent No. 6121015  
; GENERAL INFORMATION:  
; APPLICANT: O'Malley, Karen L  
; APPLICANT: Todd, Richard D  
; TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor  
; FILE REFERENCE: WU 102 CON DIV  
; CURRENT APPLICATION NUMBER: US/08/475,742  
; CURRENT FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: US 08/261,293  
; EARLIER FILING DATE: 1994-06-16  
; EARLIER APPLICATION NUMBER: US 08/014,013  
; EARLIER FILING DATE: 1993-01-28  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3907  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(3907)  
; OTHER INFORMATION: Rat D4 Gene  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(820)  
; OTHER INFORMATION: 5' flanking sequence to end of exon 1  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (821)..(2299)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2300)..(2406)  
; OTHER INFORMATION: exon  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2407)..(2499)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2500)..(3071)  
; OTHER INFORMATION: exon  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3072)..(3263)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (3264)..(3907)  
; OTHER INFORMATION: Exon 4 and 3' flanking sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (445)..(447)  
; OTHER INFORMATION: Start codon (Initiator methionine)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (3463)..(3465)  
; OTHER INFORMATION: Stop codon (TGA)  
; PUBLICATION INFORMATION:  
; AUTHORS: O'Malley, K. L.  
; AUTHORS: Harmon, S.  
; AUTHORS: Tang, S.  
; AUTHORS: O'Malley, K. L.  
; TITLE: The rat dopamine D4 receptor: sequence, gene structure  
; TITLE: and demonstration of expression in the cardiovascular  
; TITLE: system  
; JOURNAL: New Biol.  
; VOLUME: 4  
; PAGES: 1-9  
; DATE: 1992  
US-08-475-742-1

Query Match 6.4%; Score 31.6; DB 3; Length 3907;  
Best Local Similarity 48.4%; Pred. No. 0.92;  
Matches 88; Conservative 0; Mismatches 94; Indels 0; Gaps 0;  
Qy 271 tctgtctctacagctctaaatgagggggcaatatgctggaagagccacctgtgttt 330  
Db 2989 tgcgcgctctcccgagaaagagcgccaagatcactggaaggagcgcaagcgcat 3048  
Qy 331 gatgtctctacatgtattctggaacctgtgctcttcccaagaatacacagagctt 390  
Db 3049 gagagtcctgcgctggtggtgtggtgttccgcctccggagacagagctgatagaggga 3108  
Qy 391 aagaaccgtggtcttgatgataagggtggaagtaataatggaagacagccgg 450  
Db 3109 ggggtcccgaggcgagggaggagggtccagttggaaggtggaaggtgg 3168  
Qy 451 gg 452  
Db 3169 gg 3170  
RESULT 9  
US-08-045-806-3  
; Sequence 3, Application US/08045806  
; Patent No. 5378822  
; GENERAL INFORMATION:  
; APPLICANT: Bradfield, Christopher Alan  
; APPLICANT: Dolwick, Kristin Marie  
; APPLICANT: Poland, Alan  
; TITLE OF INVENTION: Ah Receptor cDNA and Method of  
; TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut  
; STREET: 100 South Wacker Drive, Suite 960  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-4002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/045,806  
; FILING DATE: 19930408  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fentress, Susan B.  
; REGISTRATION NUMBER: 31,327  
; REFERENCE/DOCKET NUMBER: NU-9207  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)-456-8000  
; TELEFAX: (312)-456-7776  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5261 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 383..2927  
US-08-045-806-3

Query Match 6.4%; Score 31.4; DB 1; Length 5261;  
Best Local Similarity 50.2%; Pred. No. 1.3; Indels 1; Gaps 1;  
Matches 103; Conservative 0; Mismatches 101; Indels 1; Gaps 1;  
Qy 6 tccaacggtaggataataatcagggtctaataagaacaaccttatgttctctcactatgt 65





```

RESULT 14
US-08-167-854-1/c
; Sequence 1, Application US/08167854
; Patent No. 5952487
; GENERAL INFORMATION:
; APPLICANT: Phillip, Wolfgang
; APPLICANT: Sapp, Martin
; APPLICANT: Cole, Stewart
; APPLICANT: Honore, Nadine
; TITLE OF INVENTION: DNA Sequencing
; TITLE OF INVENTION: HPV42-Use i
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-D
; SOFTWARE: PatentIn Release #1

```

RESULT 15  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 8999149

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
```

```
Query Match      6.2%; Score 30.4; DB 1; Length 7218;
Best Local Similarity 6.8%; Pred. NO. 3.2;
Matches 10; Conservative 85; Mismatches 51; Indels 0; Gaps 0;

Qy  43 cctatgttcctcctcactatgtatctgccccgcgaccaccacgcgcggtgtcaact 102
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1306 YYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYV 1365

Qy 103 ggtctttgtcactgttttgatgacctgtactgttttagttactagtgtttgccctgt 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1366 YYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYVYYV 1425

Qy 163 atcaccttggacagatttctgaaat 188
      : : : : : | | | | | | |
Db 1426 YYYVYYVYYVYACCAAAATTCCTCTAT 1451
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Search completed: July 15, 2002, 08:28:01  
Job time: 6684 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 06:46:38 ; Search time 16.72 Seconds  
(without alignments)  
936.756 Million cell updates/sec

Title: US-09-898-659-2  
Perfect score: 921  
Sequence: 1 MYPTVGYNLGLMKQPVPPH.....NMDRQSGVTMPYPYHAGMTR 163

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403.5	43.8	160	2 E96710	hypothetical prote
2	365.5	39.7	224	2 G96527	protein F27J15.18
3	288	31.3	190	2 A96562	unknown protein [i
4	270.5	29.4	174	2 G96710	hypothetical prote
5	193	21.0	244	2 E84885	hypothetical prote
6	164	17.8	242	2 F84788	hypothetical prote
7	123	13.4	447	2 T04702	hypothetical prote
8	115	12.5	417	2 D84556	hypothetical prote
9	104.5	11.3	230	2 T02853	hypothetical prote
10	98.5	10.7	460	2 F64752	probable melibiose
11	95.5	10.4	782	2 A61625	tenasin-like prot
12	92.5	10.0	962	2 JC5571	subtilisin-like pr
13	91	9.9	969	1 A39490	subtilisin-like pr
14	91	9.9	975	2 JC5570	subtilisin-like pr
15	87.5	9.5	1134	1 JN0711	protein-tyrosine k
16	84	9.1	232	2 D96663	unknown protein. 5
17	82.5	9.0	156	1 F69857	conserved hypothet
18	82.5	9.0	1136	1 S7845	protein-tyrosine k
19	82.5	9.0	3084	1 MMMSA	laminin alpha-1 ch
20	81	8.8	300	2 S40837	formate dehydrogen
21	81	8.8	300	2 C91231	formate dehydrogen
22	81	8.8	300	2 B86078	formate dehydrogen
23	81	8.8	300	2 AC0946	formate dehydrogen
24	81	8.8	1122	2 I54237	protein-tyrosine k
25	81	8.8	1123	1 JN0712	protein-tyrosine k
26	81	8.8	1125	1 JH0771	protein-tyrosine k
27	79.5	8.6	239	2 T16829	hypothetical prote
28	79.5	8.6	3712	2 S18253	laminin alpha-1 ch
29	78	8.5	498	2 D83994	xylose kinase xylB

30	77.5	8.4	1138	1 S24066	protein-tyrosine k
31	76	8.3	1820	2 A55494	latent transformin
32	76	8.3	3075	2 S14458	laminin alpha-1 ch
33	75.5	8.2	439	2 A36385	surface antigen se
34	75.5	8.2	2195	2 T34264	hypothetical prote
35	75.5	8.2	2471	2 A49128	cell-rate determin
36	75	8.1	1124	1 I58388	protein-tyrosine k
37	75	8.1	3507	2 T34513	hypothetical prote
38	74	8.0	238	2 B84167	glucose-1-phosphat
39	74	8.0	435	2 I54182	tumor necrosis fac
40	73.5	8.0	220	2 S42879	nodulin-30 - kidne
41	73.5	8.0	380	2 D44490	retrovirus-related
42	73.5	8.0	640	1 A30452	uromodulin precurs
43	73.5	8.0	932	2 I52527	PACE4A - mouse (fr
44	73.5	8.0	937	2 I53282	gene PACE4 protein
45	73.5	8.0	1574	2 T13954	MEGF6 protein - ra

ALIGNMENTS

RESULT 1

E96710

hypothetical protein F24J5.15 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: E96710

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: E96710

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-160 <STO>

A:Cross-references: GB:AF005173; NID:95734716; PIDN:AAD49981.1; GSPDB:GN00141

C:Genetics:

A:Gene: F24J5.15

A:Map position: 1

Query Match	43.8%	Score	403.5	DB	2	Length	160
Best Local Similarity	48.5%	Pred. No.	3.9e-31				
Matches	80	Conservative	27	Mismatches	41	Indels	17
Gaps	6						
Qy	8	NLGLMKQPVVPPHYVSAPCTTAR--WSTGLCHCFDDPANCLVTSVCPTITGQISEILNK	66				
Db	2	NLSSNDQP-----SOGRIKAKDNDLCECMNDINSCCLTCWCPCVAGRIAEVDVR	53				
Qy	67	GTTSCGSGRGLYCLL-GLTGL--PSLYSCFYRSKMRGQDLEAPCVCLVHVFCPCAL	123				
Db	54	GSTSCGVSGAMWIIIFMLTGYGSSLYSCFYRTKLRAQYNLKERPCDCCVHFCCEPCAL	113				
Qy	124	COETRELK-NGFDMGICGQANMDQRQSR-----GVTMPYPYHAGMTR	163				
Db	114	COEYRQLQHNRLDLVIGWGHGNERHARLAASTPSAPPLQAPMSR	158				

RESULT 2

G96527

protein F27J15.18 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: G96527

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,







C;Accession: A81463; T02853  
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;  
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999  
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c  
A;Reference number: A81455; MUID:99178987  
A;Accession: A81463  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-230 <PVL>  
A;Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24676.1; PID:g2266921; GSPDB:GN00  
A;Experimental source: strain MHOM/IL/81/Friedlin  
C;Genetics:  
A;Gene: Li439.5  
A;Map position: 1

	Query Match	11.3%	Score 104.5;	DB 2;	Length 230;
	Best Local Similarity	25.5%;	Pred.No. 0.013;		
	Matches	35;	Conservative	21;	Mismatches 44; Indels 37; Gaps 6;
QY	32	WSTGLGCHCFDPPANCLVTSVCPCITFGQISILNKGITS-----CGSRGALYCL-LGHTG	85		
Db	75	FISGILNCHSCAVCLDLACLCMYCTASAHNFLMNDTEGLYPVC---WGFLFCVDVUGLSA	131		
QY	86	----LPS-----LYSCFYRSKMRGOYDLEA-----PCVDCLVHVF	117		
Db	132	VSSYLPSLLPHHTYFMSAIRRRYNLHSAGAPVNSNTHGSSSGCDCTTESMLDLLLTVPF	191		
QY	118	CEPACLCQEYRELKNRG	134		
Db	192	CLPCAIAQHOREINHOG	208		

```

RESULT 10
F64752
probable melibiose carrier protein yagG - Escherichia coli
N;Alternate names: probable membrane protein yagG
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
C;Accession: F64752
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: F64752
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-460 <BLAT>

```

```

C; Gene: yagG
C; Superfamily: melibiose carrier protein
F: 80-96/Domain: transmembrane #status predicted <TMM1>
F: 107-123/Domain: transmembrane #status predicted <TMM2>
F: 155-171/Domain: transmembrane #status predicted <TMM3>
F: 184-200/Domain: transmembrane #status predicted <TMM4>
F: 298-314/Domain: transmembrane #status predicted <TMM5>
F: 317-333/Domain: transmembrane #status predicted <TMM6>
F: 371-387/Domain: transmembrane #status predicted <TMM7>
F: 406-422/Domain: transmembrane #status predicted <TMM8>

Query Match 10.7%; Score 98.5; DB 2; Length 460;
Best Local Similarity 29.3%; Pred. No. 0.099;
Matches 34; Conservative 18; Mismatches 51; Indels 13; Gaps 4;

QY 1 MYPTVGVNGLMKQYPVPHVSNAPGTTTA----RWSTGLCHCFDDPANCLVTS--VPCP 54
      *| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 108 SYACVTVILITLVYTFVNVDPYCAMPGVITADPKERHALQSWRRFFLAAGSLAISGIALP 167

QY 55 ITFGQISEILNKGTTCGSGRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCV 110

```

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      : :      | |      | | : | | | : | | | : | | : | |
Db 168 VS-----IIGKGDQGVYFGAM-CVLGLSGWLLVYCFTRKERTFEVQPGSSV 216

RESULT 11
A61625
tenascin-like protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jan-
C:Accession: A61625; S28463
R:Baumgartner, S.; Chiquet-Ehrismann, R.
Mech. Dev. 40, 165-176, 1993
A:title: Ten(a), a Drosophila gene related to tenascin, shows selective
A:reference number: A61625; MUID:93264270

```

A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-782 <BAU>  
A/Cross-references: EMBL:X68794  
C/Genetics:  
A/Gene: ten-a  
A/Cross-references: FlyBase:FBgn0004446  
C/Superfamily: unassigned EGF-related proteins; EGF homology  
C/Keywords: tandem repeat  
F/1-62/Domain: signal sequence #status predicted <SIG>  
F/63-782/Product: tenascin-like protein #status predicted <MAT>  
F/497-524/Domain: EGF homology <EGF>

Query Match	10.4%	Score 95.5;	DB 2;	Length 782;
Best Local Similarity	22.3%;	Pred. No. 0.32;		
Matches	44;	Conservative	15;	Mismatches 67; Indels 71; Gaps 9;
Qy	17	VPPHYVSAPGTTT-ARWSTGLCHC-----FDDPANCLVTSVCPCITFGQISELNKGT	68	
	:	: : :	: : :	:
Db	492	IPVGECEVPNCSSHGRCIEBECHECERGWKGPGYCDQHCL-----DPLCSGH	537	
	:	: : :	: : :	:
Qy	69	TSCGSRGALCYLLGLTL-----PSLYSFYRKMRGYDLLEAPCV-----	110	
	:	: : :	: : :	:
Db	538	GTCVA-QGCYCCKAGOWEGDCGTIDQQVYQLPGCSEHGYDLETGQCVCERHWTGPDCSQ	596	
	:	: : :	: : :	:
Qy	111	-----DCLVHVHFBC-----PC-ALCOEYRELKNRFGDMGTGWQNMD	146	
	:	: : :	: : :	:
Db	597	AVCSLDCGRNVCESGKCRCNSGWTGNLCDDLPDCDSRCSHGQKNGTCVCSOGW-----	651	
	:	: : :	: : :	:
Qy	147	RQSRGVTPMPYPYHAGMTR	163	
	:	: . : :	: . : :	:
Db	652	-NGRHCTLPGCCNGCSR	667	

RESULT 12

JC5571  
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-II  
C:Species: Homo sapiens (man)  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000  
C:Accession: JC5571  
R:Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.;  
J. Biochem. 121, 941-948, 1997  
A:Title: A novel human PACE4 isoform, PACE4E is an active processing protease contain  
A:Reference number: JC5570; MUID:97335942  
A:Accession: JC5571  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-962 <MOR>  
A:Cross-references: DDBJ:D87994; NID:G2330550; PIDN:BAA21792.1; PID:G2330551  
A:Experimental source: brain cerebellum  
C:Comment: This enzyme is a processing protease and responsible for processing of var  
ch. it is retained intracellularly.  
C:Genetics:  
A:Gene: GDB:PACE4  
A:Cross-references: GDB:131390; OMIM:167405  
A:Map position: 15q26-15q26  
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology



A:Cross-references: EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611  
 R:Sato, T.N.; Qin, Y.; Kozak, C.A.; Audus, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 9355-9358, 1993  
 A:Title: tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes  
 A:Reference number: S57845; MUID:94022374  
 A:Accession: S57847  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-598, 'L', 600-1134 <SA2>  
 A:Cross-references: EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993  
 R:Korhonen, J.; Partanen, J.; Armstrong, E.; Vahtokari, A.; Elenius, K.; Jalakanen, M.;  
 Blood 80, 2548-2555, 1992  
 A:Title: Enhanced expression of the tie receptor tyrosine kinase in endothelial cells du  
 A:Reference number: A48926; MUID:93043301  
 A:Accession: A48926  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 221-352/740-890 <KOR>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:118660, NCBIP:118662)  
 R:Korhonen, J.; Lahtinen, I.; Halmekyto, M.; Alhonen, L.; Janne, J.; Dumont, D.; Alitalo  
 Blood 86, 1828-1835, 1995  
 A:Title: Endothelial-specific gene expression directed by the tie gene promoter in vivo.  
 A:Reference number: I52613; MUID:95383653  
 A:Accession: I63403  
 A:Status: preliminary; translated from GB/EMBL/DD9J  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:S79346; NID:g1086920  
 C:Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin tyf  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-1134/Product: protein-tyrosine kinase, receptor type tie #status predicted <MAT>  
 F;36-105/Domain: immunoglobulin homology <IM1>  
 F;213-253/Domain: EGF homology <EG1>  
 F;257-300/Domain: EGF homology <EG2>  
 F;304-342/Domain: EGF homology <EG3>  
 F;363-426/Domain: immunoglobulin homology <IM2>  
 F;447-528/Domain: fibronectin type III repeat homology <FN3A>  
 F;540-629/Domain: fibronectin type III repeat homology <FN3B>  
 F;638-726/Domain: fibronectin type III repeat homology <FN3C>  
 F;757-782/Domain: transmembrane #status predicted <TM>  
 F;833-1110/Domain: protein kinase homology <KIN>  
 F;841-849/Region: protein kinase ATP-binding motif  
 F;43-103,370-424/Disulfide bonds: #status predicted  
 F;81,159,501,592,705/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;866,883,975/Active site: Lys, Glu, Asp #status predicted

Query Match 9.5%; Score 87.5; DB 1; Length 1134;  
 Best Local Similarity 26.2%; Pred. No. 2.7;  
 Matches 34; Conservative 7; Mismatches 48; Indels 41; Gaps 8;  
 QY 26 GTTTARWSTGLCHCFDDPANCLVTSVC-----PCI-----TFGQISEI 63  
 Db 212 GCAGAGRWPG---CVKDCPGCLHGGVHDGECVPGPTGTRCQACREGRFQSCQE 268  
 QY 64 LNRGTTSCGSRGALYCLLGLTSLYSCFYRSKMRQYDLEAPC-----VDCLVHVF 117  
 Db 269 QCFGTAGC--RGLTFC-----LPDPYGCSCGSGWRGS-QCQEA-CAPDFGADCRLOQC 318  
 QY 118 CEPCLQCQY 127  
 Db 319 CQNGGTCDFR 328

Search completed: July 15, 2002, 06:48:13  
 Job time: 95 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 06:47:53 ; Search time 11.96 Seconds  
(without alignments)  
527.700 Million cell updates/sec

Title: US-09-898-659-2

Perfect score: 921

Sequence: 1 MYPTVGYNLGLMKQYVPPH.....NMDRSGVTWPPYHAGMTR 163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98.5	10.7	460	1 YAGG_ECOLI	P75683 escherichia
2	91	9.9	969	1 PAC4_HUMAN	P29122 homo sapien
3	87.5	9.5	1134	1 TIE1_MOUSE	Q06806 mus musculus
4	84	9.1	626	1 HCYB_EURCA	Q9nfh9 eurytelma c
5	82.5	9.0	1136	1 TIE1_BOVIN	Q06805 bos taurus
6	82.5	9.0	3084	1 LMA1_MOUSE	P19137 mus musculus
7	81	8.8	300	1 FDOH_ECOLI	P32175 escherichia
8	81	8.8	1122	1 TIE2_MOUSE	Q02858 mus musculus
9	79.5	8.6	3712	1 LMA_DROME	Q00174 drosophila
10	77.5	8.4	798	1 ITB5_MOUSE	O70309 mus musculus
11	77.5	8.4	1138	1 TIE1_HUMAN	P35590 homo sapien
12	77	8.4	1376	1 CRBH_HUMAN	P82279 homo sapien
13	76	8.3	3075	1 LMA1_HUMAN	P25391 homo sapien
14	75	8.1	1124	1 TIE2_HUMAN	Q02763 homo sapien
15	74.5	8.1	857	1 ENV_HV2RR	Q74126 human immun
16	74.5	8.1	3110	1 LMA2_HUMAN	P24043 homo sapien
17	74	8.0	435	1 TNR3_HUMAN	P36941 homo sapien
18	73.5	8.0	383	1 P013_NASVI	Q03271 nasonia vit
19	73.5	8.0	640	1 UROM_HUMAN	P07911 homo sapien
20	73.5	8.0	937	1 PAC4_RAT	Q63415 rattus norv
21	72.5	7.9	914	1 PERT_MOUSE	P35419 mus musculus
22	72.5	7.9	1104	1 NF31_HUMAN	Q12986 homo sapien
23	72	7.8	460	1 HYIN_ERWHE	Q47860 erwinia her
24	72	7.8	933	1 PRGR_HUMAN	P06401 homo sapien
25	72	7.8	1801	1 LMB2_RAT	P15800 rattus norv
26	71.5	7.8	755	1 COMP_RAT	P35444 rattus norv
27	71.5	7.8	3106	1 LMA2_MOUSE	Q06075 mus musculus
28	71	7.7	529	1 NRDI_SCHPO	Q09702 schizosacch
29	71	7.7	615	1 FA12_HUMAN	Q00748 homo sapien
30	71	7.7	1592	1 SORL_CHICK	Q98930 g sortilin-
31	70.5	7.7	259	1 PURA_ACTAC	P96771 actinobacil
32	70.5	7.7	1786	1 LMB1_HUMAN	P07942 homo sapien
33	70	7.6	591	1 UL49_EBV	P14347 Epstein-Bar

#### RESULT 1

ID	YAGG_ECOLI	STANDARD;	PRT;	460 AA.
DT	P75683; P71292;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-Oct-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical symporter yagg.			
GN	YAGG OR B0270.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1455-1474(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,			
RA	Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,			
RA	Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,			
RA	Davis R.W.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane			
CC	(Potential).			
CC	-!- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY			
CC	(SGF). STRONG, TO E.COLI Y1G1.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AE000135; AAC73373.1; -			
DR	EMBL; U70214; AAB08691.1; -			
DR	ECOGene; EG13346; yagg.			
DR	InterPro: IPR001927; Na_galact_symp.			
DR	Pfam: PF01236; Na_Galact_symp; 1			
DR	PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.			
KW	Hypothetical protein; Transport; Transmembrane; Inner membrane;			
KW	Symport; Complete proteome.			
FT	TRANSMEM 10 30 POTENTIAL.			
FT	TRANSMEM 31 51 POTENTIAL.			
FT	TRANSMEM 79 99 POTENTIAL.			
FT	TRANSMEM 107 127 POTENTIAL.			
FT	TRANSMEM 151 171 POTENTIAL.			

Q00175 mus musculus  
Q63449 rattus norv  
P31696 gallus gall  
P78369 homo sapien  
P13508 caenorhabdi  
Q05793 mus musculus  
P76055 escherichia  
P25266 herpetosiph  
P12336 rattus norv  
P01874 canis famil  
Q07327 drosophila  
Q14202 homo sapien

#### ALIGNMENTS

34 70 7.6 923 1 PRGR\_MOUSE  
35 70 7.6 923 1 PRGR\_RAT  
36 70 7.6 1955 1 AGR1\_CHICK  
37 69.5 7.5 228 1 CLDA\_HUMAN  
38 69 7.5 1295 1 GLPI\_CAEEL  
39 69 7.5 3707 1 PGBM\_MOUSE  
40 68.5 7.4 311 1 YDAO\_ECOLI  
41 68.5 7.4 437 1 MTEI\_HERAU  
42 68.5 7.4 522 1 GTR2\_RAT  
43 68 7.4 450 1 MUC\_CANFA  
44 68 7.4 597 1 ROP\_DROME  
45 68 7.4 1370 1 Z261\_HUMAN

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FT TRANSMEM 180 200 POTENTIAL.
FT TRANSMEM 263 283 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
FT TRANSMEM 367 387 POTENTIAL.
FT TRANSMEM 406 426 POTENTIAL.
FT CONFLICT 370 370 K -> N (IN REF. 2).
SQ SEQUENCE 460 AA; 50631 MW; AB600588E663C6B7 CRC64;

Query Match 10.7%; Score 98.5; DB 1; Length 460;
Best Local Similarity 29.3%; Pred. No. 0.014;
Matches 34; Conservative 18; Mismatches 51; Indels 13; Gaps 4;

QY 1 MYPTGVNIGLMKQPVYPHYVSAPGTTTA----RWSTGLCHCFDDPANCLVTS--VCP 54
:| | | | :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 108 IYACVTVYILLTVYTVNVPYCAMPGVITADPKERHALQSRFFLAAGSLAISGIALPL 167

QY 55 IFPGQISEILNKGTTSCGSRGALYCLLLGLTGLPSLYSCYFRSKMRQYDLEAPCV 110
: : : : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 168 VS-----IIGKDEQGVYFGAM-CVLGLSGVLLYVCFEFTTKERYTFEVQPGSSV 216

RESULT 2
PAC4_HUMAN STANDARD; PRT; 969 AA.
ID PAC4_HUMAN Q9UEJ7; Q9UEJ2; Q9UEJ7; Q9UEJ8; Q9UEJ9;
AC Q9UEG7; Q9Y4G9; Q9Y4H0; Q9Y4H1;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
DE (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
DE convertase 4) (SPC4).
GN PACE4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
RC TISSUE=Hepatoma, and Kidney;
RX MEDLINE=92075167; PubMed=1741956;
RA Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
RA Barr P.J.;
RT "Identification of a second human subtilisin-like protease gene in
RT the fes/fps region of chromosome 15.";
RL DNA Cell Biol. 10:757-769(1991).
[2]
SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
RC TISSUE=Placenta;
RX MEDLINE=94235049; PubMed=8179631;
RA Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
RA Matsuda Y.;
RT "Identification of novel cDNAs encoding human kexin-like protease,
RT PACE4 isoforms.";
RL Biochem. Biophys. Res. Commun. 200:943-950(1994).
[3]
ERRATUM.
RX MEDLINE=95071480; PubMed=7980617;
RA Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
RA Matsuda Y.;
RT "Identification of novel cDNAs encoding human kexin-like protease,
RT PACE4 isoforms.";
RL Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
[4]
SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
RC TISSUE=Placenta;
RX Mori K., Inamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
RA Matsuda Y.;
RT "Identification of a novel PACE4 isoform, PACE4E.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE, FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
```

```
RC TISSUE=Cerebellum;
RX MEDLINE=97335942; PubMed=9192737;
RA Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
RA Akamatsu T., Nagamune H., Matsuda Y.;
RT "A novel human PACE4 isoform, PACE4E is an active processing protease
RT containing a hydrophobic cluster at the carboxy terminus.";
RL J. Biochem. 121:941-948(1997).
[6]
SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
RX MEDLINE=98021085; PubMed=9378725;
RA Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
RA Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.;
RT "Genomic organization and alternative splicing of human PACE4 (SPC4),
RT kexin-like processing endoprotease.";
RL J. Biochem. 122:438-452(1997).
[7]
ALTERNATIVE SPLICING (ISOFORM PACE4CS).
RX MEDLINE=97064242; PubMed=8906861;
RA Zhong M., Benjannet S., Lazure C., Munzer S., Seldah N.G.;
RT "Functional analysis of human PACE4-A and PACE4-C isoforms:
RT identification of a new PACE4-CS isoform.";
RL FEBS Lett. 396:31-36(1996).
[8]
CHARACTERIZATION.
RX MEDLINE=99233559; PubMed=10215603;
RA Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
RA Moehring T.J.;
RT "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and
RT can partly rescue the phenotype of a furin-deficient cell strain.";
RL Biochem. J. 339:639-647(1999).
[9]
PROCESSING.
RX MEDLINE=98408849; PubMed=9738469;
RA Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,
RA Tsuji A., Matsuda Y.;
RT "Biosynthetic processing and quaternary interactions of proprotein
RT convertase SPC4 (PACE4).";
RL FEBS Lett. 434:155-159(1998).
[1]
FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTASE ACTIVITY WITHIN THE
CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
[2]
CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
PROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS,
WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
[3]
COFACTOR: PACE4A IS PROBABLY CALCIUM-DEPENDENT.
[4]
SUBUNIT: THE PACE4A-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE
RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT
PROPEPTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.
[5]
SUBCELLULAR LOCATION: PACE4A-I AND PACE4-AII ARE SECRETED. PACE4C
AND PACE4CS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM
IN ENDOPLASMIC RETICULUM. PACE4E-I AND PACE4E-II ARE RETAINED
INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
TERMINUS. PACE4B MIGHT BE SECRETED.
[6]
ALTERNATIVE PRODUCTS: 8 ISOFORMS: PACE4A-I/PACE4 (SHOWN HERE),
PACE4A-II, PACE4B/PACE4.1, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
[7]
TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
CEREBELLUM.
[8]
DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
RETICULUM. ISOFORM PACE4D LACKS THE PROPEPTIDE DOMAIN.
[9]
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
SUBTILASE FAMILY.
```









OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=89034134; PubMed=318280;  
RA Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;  
RT "Laminin, a multidomain protein. The A chain has a unique globular  
RT domain and homology with the basement membrane proteoglycan and the  
RT laminin B chains";  
RL J. Biol. Chem. 263:16536-16544(1988).  
RN [2]  
RP SEQUENCE OF 1-339 FROM N.A.  
RX MEDLINE=88225080; PubMed=3267223;  
RA Hartl L., Oberbaumer I., Deutzmann R.;  
RT "The N terminus of laminin A chain is homologous to the B chains.";  
RL Eur. J. Biochem. 173:629-635(1988).  
RN [3]  
RP SEQUENCE OF 2538-3084 FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=89030693; PubMed=3181157;  
RA Deutzmann R., Huber J., Schmetz K.A., Oberbaumer I., Hartl L.;  
RT "Structural study of long arm fragments of laminin. Evidence for  
RT repetitive C-terminal sequences in the A-chain, not present in the B-  
RT chains";  
RL Eur. J. Biochem. 177:35-45(1988).  
RN [4]  
RP FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC [5]  
RP SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND  
CC LAMININ-3 (S-LAMININ).  
CC [6]  
RP SUBCELLULAR LOCATION: Extracellular.  
CC [7]  
RP TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT).  
CC [8]  
RP DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC [9]  
RP SIMILARITY: CONTAINS 17 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC [10]  
RP SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.  
CC [11]  
RP SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.  
CC [12]  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC [13]  
RP EMBL: J04064; AAA39410.1; -  
DR EMBL: X07737; CAA30561.1; -  
DR EMBL: X13459; CAA31807.1; -  
DR EMBL: M36775; AAA39406.1; -  
DR PIR: A31771; WMSA.  
DR HSSP: P02458; 1TLE.  
DR MGD: MGI:99892; Lamal.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR001886; LamNT.  
DR InterPro: IPR000034; Laminin\_B.  
DR InterPro: IPR002049; Laminin\_EGF.  
DR InterPro: IPR001791; Laminin\_G.  
DR Pfam: PF00052; laminin\_B; 2.  
DR Pfam: PF00053; laminin\_EGF; 15.  
DR Pfam: PF00054; laminin\_G; 5.  
DR Pfam: PF00055; laminin\_Nterm; 1.  
DR PRINTS: PRO0011; EGFLAMIN.  
DR ProDom: PD002082; LamNT; 1.  
DR ProDom: PD003031; Laminin\_B; 2.  
DR SMART: SM00180; EGF\_Lam; 14.  
DR SMART: SM00281; LamB; 2.  
DR SMART: SM00282; LamG; 5.  
DR SMART: SM00136; LamNT; 1.  
DR PROSITE: PS00022; EGF\_1; 11.  
DR PROSITE: PS01186; EGF\_2; 3.  
DR PROSITE: PS01248; LAMININ\_TYPE\_EGF; 15.  
DR PROSITE: PS00025; LAM\_G\_DOMAIN; 5.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 3084 LAMININ ALPHA-1 CHAIN.  
FT MOD\_RES 25 25 BLOCKED.  
FT DOMAIN 25 276 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 277 333 LAMININ EGF-LIKE 1.  
FT DOMAIN 334 403 LAMININ EGF-LIKE 2.  
FT DOMAIN 404 460 LAMININ EGF-LIKE 3.  
FT DOMAIN 461 509 LAMININ EGF-LIKE 4.  
FT DOMAIN 510 519 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 520 715 LAMININ DOMAIN IV 1 (DOMAIN IV B).  
FT DOMAIN 716 748 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 749 797 LAMININ EGF-LIKE 6.  
FT DOMAIN 798 855 LAMININ EGF-LIKE 7.  
FT DOMAIN 856 908 LAMININ EGF-LIKE 8.  
FT DOMAIN 909 957 LAMININ EGF-LIKE 9.  
FT DOMAIN 958 1004 LAMININ EGF-LIKE 10.  
FT DOMAIN 1005 1050 LAMININ EGF-LIKE 11.  
FT DOMAIN 1051 1096 LAMININ EGF-LIKE 12.  
FT DOMAIN 1097 1156 LAMININ EGF-LIKE 13.  
FT DOMAIN 1157 1368 LAMININ EGF-LIKE 14 (N-TERMINAL).  
FT DOMAIN 1369 1409 LAMININ DOMAIN IV 2 (DOMAIN IV A).  
FT DOMAIN 1410 1458 LAMININ EGF-LIKE 14 (C-TERMINAL).  
FT DOMAIN 1459 1515 LAMININ EGF-LIKE 15.  
FT DOMAIN 1516 1562 LAMININ EGF-LIKE 16.  
FT DOMAIN 1563 1612 LAMININ EGF-LIKE 17.  
FT DOMAIN 1612 1820 LAMININ II AND I.  
FT DOMAIN 1820 1869 LAMININ G-LIKE 1.  
FT DOMAIN 1869 1903 LAMININ G-LIKE 2.  
FT DOMAIN 1903 2096 LAMININ G-LIKE 3.  
FT DOMAIN 2096 2128 LAMININ G-LIKE 4.  
FT SITE 1147 1149 LAMININ G-LIKE 5.  
FT DISULFID 277 286 COILED COIL (POTENTIAL).  
FT DISULFID 279 297 COILED COIL (POTENTIAL).  
FT DISULFID 299 308 COILED COIL (POTENTIAL).  
FT DISULFID 311 331 CELL ATTACHMENT SITE.  
FT DISULFID 334 343 BY SIMILARITY.  
FT DISULFID 336 368 BY SIMILARITY.  
FT DISULFID 371 380 BY SIMILARITY.  
FT DISULFID 383 401 BY SIMILARITY.  
FT DISULFID 404 416 BY SIMILARITY.  
FT DISULFID 406 434 BY SIMILARITY.  
FT DISULFID 436 445 BY SIMILARITY.  
FT DISULFID 448 458 BY SIMILARITY.  
FT DISULFID 461 474 BY SIMILARITY.  
FT DISULFID 463 478 BY SIMILARITY.  
FT DISULFID 480 489 BY SIMILARITY.  
FT DISULFID 492 507 BY SIMILARITY.  
FT DISULFID 749 758 BY SIMILARITY.  
FT DISULFID 751 764 BY SIMILARITY.  
FT DISULFID 767 776 BY SIMILARITY.  
FT DISULFID 779 795 BY SIMILARITY.  
FT DISULFID 798 813 BY SIMILARITY.  
FT DISULFID 800 823 BY SIMILARITY.  
FT DISULFID 826 835 BY SIMILARITY.  
FT DISULFID 838 853 BY SIMILARITY.  
FT DISULFID 856 870 BY SIMILARITY.  
FT DISULFID 877 889 BY SIMILARITY.  
FT DISULFID 890 899 BY SIMILARITY.

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FT DISULFID 892 906 BY SIMILARITY.
FT DISULFID 909 921 BY SIMILARITY.
FT DISULFID 911 928 BY SIMILARITY.
FT DISULFID 930 939 BY SIMILARITY.
FT DISULFID 942 955 BY SIMILARITY.
FT DISULFID 958 970 BY SIMILARITY.
FT DISULFID 960 976 BY SIMILARITY.
FT DISULFID 978 987 BY SIMILARITY.
FT DISULFID 990 1002 BY SIMILARITY.
FT DISULFID 1005 1014 BY SIMILARITY.
FT DISULFID 1007 1021 BY SIMILARITY.
FT DISULFID 1023 1032 BY SIMILARITY.
FT DISULFID 1035 1048 BY SIMILARITY.
FT DISULFID 1051 1063 BY SIMILARITY.
FT DISULFID 1053 1070 BY SIMILARITY.
FT DISULFID 1072 1081 BY SIMILARITY.
FT DISULFID 1084 1094 BY SIMILARITY.
FT DISULFID 1100 1119 BY SIMILARITY.
FT DISULFID 1121 1138 BY SIMILARITY.
FT DISULFID 1142 1158 BY SIMILARITY.
FT DISULFID 1161 1179 BY SIMILARITY.
FT DISULFID 1181 1198 BY SIMILARITY.
FT DISULFID 1201 1219 BY SIMILARITY.
FT DISULFID 1231 1248 BY SIMILARITY.
FT DISULFID 1251 1268 BY SIMILARITY.
FT DISULFID 1271 1288 BY SIMILARITY.
FT DISULFID 1291 1308 BY SIMILARITY.
FT DISULFID 1311 1328 BY SIMILARITY.
FT DISULFID 1331 1348 BY SIMILARITY.
FT DISULFID 1351 1368 BY SIMILARITY.
FT DISULFID 1371 1388 BY SIMILARITY.
FT DISULFID 1391 1408 BY SIMILARITY.
FT DISULFID 1411 1428 BY SIMILARITY.
FT DISULFID 1431 1448 BY SIMILARITY.
FT DISULFID 1451 1468 BY SIMILARITY.
FT DISULFID 1471 1488 BY SIMILARITY.
FT DISULFID 1491 1508 BY SIMILARITY.
FT DISULFID 1511 1528 BY SIMILARITY.
FT DISULFID 1531 1548 BY SIMILARITY.
FT DISULFID 1551 1568 BY SIMILARITY.
FT DISULFID 1563 1576 INTERCHAIN (PROBABLE).
FT DISULFID 1567 1567 INTERCHAIN (PROBABLE).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 531 531 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 770 770 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 857 857 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 959 959 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 969 969 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1052 1052 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1344 1344 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1414 1414 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1586 1586 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 9.08; Score 82.5; DB 1; Length 3084;
Best Local Similarity 29.48; Pred. No. 4.2;
Matches 40; Conservative 10; Mismatches 57; Indels 29; Gaps 9;

OY 4 TVGYNLGLMKQYPVPHVSVAPGTTTARWSTGLCHCFDDPANCLVTSVCPCTTFOGISEI 63
DB 375 TTGINCEICIDQYRPHKVSYPDDHPCR-----PCNC--DPVGSLSV-CIKDDRHADL 425
OY 64 LN-KGTTSCGRGAL-----YCLGLGLPLSLYSCFYRSKMRGYDLEAPVCDLVHV 116
DB 426 ANGKWPQCPCKRGYAGDKDCRCQFGYRFPNCIPC-----DCRTVGLSLNEDPCI----- 475
OY 117 FCEPCALQCEYRELKN 132
DB 476 --EPC-LCKKNVEGKN 488

RESULT 7
FDOH_ECOLI
ID FDOH_ECOLI STANDARD: PRT; 300 AA.
AC P32175;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Formate dehydrogenase-O, Iron-sulfur subunit (Formate dehydrogenase-O
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DE beta subunit) (FDH-2 beta subunit) (Aerobic formate dehydrogenase
DE iron-sulfur subunit).
GN FDOH OR B3893.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RC MEDLINE=93347969; PubMed=8346018;
RX Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RA "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes.";
RL Nucleic Acids Res. 21:3391-3398(1993).
RN [2]
RN CHARACTERIZATION.
RC STRAIN-K12;
RC MEDLINE=96099298; PubMed=8522521;
RX Aibaou H., Pommier J., Giordano G., Mandrand-Berthelot M.-A.;
RA "Expression and characterization of the Escherichia coli fdo locus
RT and a possible physiological role for aerobic formate
RT dehydrogenase.";
RN J. Bacteriol. 177:7141-7149(1995).
RN [3]
RN TOPOLOGY.
RC MEDLINE=99069333; PubMed=9852007;
RX Benoit S., Aibaou H., Mandrand-Berthelot M.-A.;
RA "Topological analysis of the aerobic membrane-bound formate
RT dehydrogenase of Escherichia coli.";
RN J. Bacteriol. 180:6625-6634(1998).
CC -1- FUNCTION: ALLOWS TO USE FORMATE AS MAJOR ELECTRON DONOR DURING
CC AEROBIC RESPIRATION. THE BETA CHAIN IS AN ELECTRON TRANSFER UNIT
CC CONTAINING 4 CYSTEINE CLUSTERS INVOLVED IN THE FORMATION OF IRON-
CC SULFUR CENTERS. ELECTRONS ARE TRANSFERRED FROM THE GAMMA CHAIN TO
CC THE MOLYBDENUM COFACTOR OF THE ALPHA SUBUNIT (BY SIMILARITY).
CC -1- SUBUNIT: FORMATE DEHYDROGENASE IS A MEMBRANE-BOUND COMPLEX, FORMED
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
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CC -----
CC EMBL; L19201; AB03026.1; -.
CC EMBL; AE000484; AAD13455.1; -.
CC PIR; S40837; S40837.
CC HSSP; P00193; 1FDX.
CC EcoGene; EG11857; fdoH.
CC InterPro; IPR001450; 4Fe4S_ferredoxin.
CC Pfam; PF00037; fer4; 1.
CC PRINTS; PR00353; 4FE4SERDOXIN.
CC PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
CC Electron transport; 4Fe-4S; Iron-sulfur; Transmembrane;
CC Complete proteome.
CC DOMAIN 1 260 CYTOPLASMIC (PROBABLE).
CC TRANSMEM 261 279 PROBABLE.
CC DOMAIN 280 300 PERIPLASMIC (PROBABLE).
CC METAL 39 39 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 42 42 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 45 45 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 49 49 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 100 100 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 103 103 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 108 108 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 112 112 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 133 133 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
CC METAL 136 136 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
CC METAL 139 139 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
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FT DOMAIN 301 341
FT DOMAIN 370 424
FT DOMAIN 444 536
FT DOMAIN 539 633
FT DOMAIN 637 731
FT DOMAIN 822 1094
FT NP_BIND 828 836
FT BINDING 853 853
FT ACT_SITE 962 962
FT CARBOHYD 140 140
FT CARBOHYD 158 158
FT CARBOHYD 399 399
FT CARBOHYD 438 438
FT CARBOHYD 464 464
FT CARBOHYD 558 558
FT CARBOHYD 595 595
FT CARBOHYD 648 648
FT CARBOHYD 690 690
FT MOD_RES 990 990
FT CONFLICT 161 171
FT CONFLICT 538 538
FT CONFLICT 736 736
FT CONFLICT 745 761
FT CONFLICT 786 786
FT CONFLICT 913 913
FT CONFLICT 925 931
FT CONFLICT 1117 1117
SQ SEQUENCE 1122 AA; 125700 MW; F879623D103FFE96 CRC64;

Query Match 8.8%; Score 81; DB 1; Length 1122;
Best Local Similarity 24.1%; Pred. No. 2.1;
Matches 32; Conservative 14; Mismatches 57; Indels 30; Gaps 7;

QY 23 SAPGTTTARWSTGLCHCFDDPANCL-----VTSVPCITFGQISILNKGTTSCGS 73
| | | | : | | | : | | | | : | | | : | | | | : | | | |
Db 221 SPPCTYCK--NGVCH--EDTGECIPPGFMGRTCEKACEPTFGTKRCSGPEGC-- 274
| | | | : | | | : | | | | : | | | : | | | | : | | | |
QY 74 RGALYCLGLTGLPSLYSCFYRSKRGQYDLEAPC-----VCLVHVFCPCALQOEYRE 129
| | | | : | | | : | | | | : | | | : | | | | : | | | |
Db 275 KSYVFC-----LPDPYGCSCATGWRGLQCNEARSGYYPGDKLRCHCTNEICDRF-- 326
| | | | : | | | : | | | | : | | | : | | | | : | | | |
QY 130 LKNRGFDMIGWQ 142
| | | | : | | | : | | | | : | | | : | | | | : | | | |
Db 327 ---QGCLCSQGWQ 336
| | | | : | | | : | | | | : | | | : | | | | : | | | |

RESULT 9
LMA_DROME STANDARD; PRT; 3712 AA.
AC Q00174;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE Laminin alpha chain precursor.
GN LANA OR LAMA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9304203; PubMed=1425596;
RA Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler J.H.;
RT "Laminin A chain: expression during Drosophila development and
genomic sequence."
RL EMBO J. 11:4519-4527(1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
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RX MEDLINE=94038678; PubMed=8223265;
RA Hencliffe C., Garcia-Alonso L., Tang J., Goodman C.S.;
RT "Genetic analysis of laminin A reveals diverse functions during
morphogenesis in Drosophila."
RL Development 118:325-337(1993).
RN [3]
RX SEQUENCE OF 1762-3712 FROM N.A.
RX MEDLINE=92078147; PubMed=1744083;
RA Garrison K., Mackrell A.J., Fessler J.H.;
RT "Drosophila laminin A chain sequence, interspecies comparison, and
domain structure of a major carboxyl portion."
J. Biol. Chem. 266:22899-22904(1991).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT, BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- FUNCTION: DIVERSE FUNCTION MUTATIONS DURING MORPHOGENESIS IN DROSOPHILA.
CC COMPLETE LOSS-OF-FUNCTION MUTATIONS LEAD TO LATE EMBRYONIC
LETHALITY. CERTAIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE
TO ESCAPER ADULTS, WHICH HAVE ROUGH EYES ASSOCIATED WITH CHANGES
IN CELL FATE AND PATTERN, MISSHAPEN LEGS AND DEFECTS IN WING
STRUCTURE.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRANES (MAJOR COMPONENT).
CC -!- TISSUE SPECIFICITY: NEWLY FORMED MESODERM AND LATER PROMINENTLY
EXPRESSED IN HEMOCYTES, WHICH ALSO SYNTHESIZE COLLAGEN IV.
CC -!- DEVELOPMENTAL STAGE: DURING MORPHOGENESIS, MOSTLY IN EMBRYO
DEVELOPMENT AT 10-12 HOURS.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV) IS NOT
SIMILAR TO LAMININ DOMAIN IV).
CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
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CC -----
DR EMBL; M96388; AAA28662.1; -.
DR EMBL; L07288; AAC37178.1; -.
DR EMBL; M75882; AAA28661.1; -.
DR HSP; P02468; 1TLE.
DR FlyBase; FBgn0002526; LANA.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001886; LamNT.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001230; Prenyltn.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 20.
DR Pfam; PF00054; laminin_G; 5.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD002082; LamNT; 1.
DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF_Lam; 17.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 17.
```

FT	DISULFID	634	650	BY SIMILARITY.
FT	DISULFID	652	661	BY SIMILARITY.
FT	DISULFID	664	674	BY SIMILARITY.
FT	DISULFID	677	691	BY SIMILARITY.
FT	DISULFID	679	700	BY SIMILARITY.
FT	DISULFID	702	711	BY SIMILARITY.
FT	DISULFID	714	729	BY SIMILARITY.
FT	DISULFID	732	746	BY SIMILARITY.
FT	DISULFID	734	753	BY SIMILARITY.
FT	DISULFID	755	764	BY SIMILARITY.
FT	DISULFID	767	782	BY SIMILARITY.
FT	DISULFID	1375	1387	BY SIMILARITY.
FT	DISULFID	1377	1394	BY SIMILARITY.
FT	DISULFID	1396	1405	BY SIMILARITY.
FT	DISULFID	1408	1418	BY SIMILARITY.
FT	DISULFID	1421	1429	BY SIMILARITY.
FT	DISULFID	1423	1436	BY SIMILARITY.
FT	DISULFID	1438	1447	BY SIMILARITY.
FT	DISULFID	1450	1463	BY SIMILARITY.
FT	DISULFID	1466	1480	BY SIMILARITY.
FT	DISULFID	1468	1487	BY SIMILARITY.
FT	DISULFID	1489	1498	BY SIMILARITY.
FT	DISULFID	1501	1511	BY SIMILARITY.
FT	DISULFID	1514	1526	BY SIMILARITY.
FT	DISULFID	1516	1533	BY SIMILARITY.
FT	DISULFID	1535	1544	BY SIMILARITY.
FT	DISULFID	1547	1562	BY SIMILARITY.
FT	DISULFID	1859	1874	BY SIMILARITY.
FT	DISULFID	1861	1885	BY SIMILARITY.
FT	DISULFID	1887	1896	BY SIMILARITY.
FT	DISULFID	1899	1914	BY SIMILARITY.

Query Match 8.6%; Score 79.5; DB 1; Length 3712;

Best Local Similarity 26.0%; Pred. No. 10; Indels 33; Gaps

Matches 34; Conservative 9; Mismatches 55;

Qy	4	TVGVNLGLMKQPYVPP	---HV---	VSAPGTTTARWSTGLCHCFDDPANC	LVTSVCP	CI 56
Db	374	TVGINCNKCPKPYRPGKHNEDVCS	QCQDYFFSTG	--HCEETGN	-----	CECRA 425
Qy	57	FGQISEILNKGTGSGRGALYCLLGLT	GLTGLPSYSCPYRSMKRGQYDLE	-----	EAP	CD 111
Db	426	AFQ	-----PPSCDS	-----	CAYGYGYGPNCRECBCLNLTNGYHCEAESG	QCPCPKI 472
Qy	112	CLVHVFEPCA	122			
Db	473	NFAGAYCKQCA	483			

RESULT 10

ITB5\_MOUSE

ID	ITB5_MOUSE	STANDARD;	PRT;	798 AA.
AC	070309; 070308; 088347;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Integrin beta-5 precursor.			
GN	ITGB5.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa;			
OC	Mammalia; Eutheria; Rodentia;			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS BETA-5A AND BETA-5B).			
RC	TISSUE=Liver;			
RX	MEDLINE=98198405; PubMed=9531507;			
RA	Zhang H., Tan S.M., Lu J.;			
RT	"cDNA cloning reveals two mouse beta5 integrin transcripts distinct i			
RL	cytoplasmic domains as a result of alternative splicing."			
RN	Biochem. J. 331:631-637(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA-5A).			
RC	TISSUE=Brain;			









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```
CC CC EMBL; AF154671; AAF01361.1; --
CC CC HSP; P08709; 1BF9.
DR DR MIM; 604210; --
DR DR MIM; 600105; --
DR DR InterPro; IPR000152; Asx_hydroxyl.
DR DR InterPro; IPR000561; EGF-like.
DR DR InterPro; IPR000742; EGF_2.
DR DR InterPro; IPR001881; EGF_Ca.
DR DR InterPro; IPR001438; EGF_11.
DR DR InterPro; IPR002049; Laminin_EGF.
DR DR InterPro; IPR001791; Laminin_G.
DR DR Pfam; PF00008; EGF; 16.
DR DR Pfam; PF00054; Laminin_G; 3.
DR DR PRINTS; PR00010; EGFBL00D.
DR DR PRINTS; PR00011; EGF_LAMININ.
DR DR SMART; SM00179; EGF_CA; 8.
DR DR SMART; SM00001; EGF_like; 8.
DR DR SMART; SM00282; LamG; 3.
DR DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR DR PROSITE; PS00022; EGF_1; 15.
DR DR PROSITE; PS01186; EGF_2; 11.
DR DR PROSITE; PS01187; EGF_CA; 7.
DR DR PROSITE; PS00025; LAM_G_DOMAIN; 3.
KW EGF-like domain; Glycoprotein; Repeat; Signal; Disease mutation;
KW Retinitis pigmentosa; Vision.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 1376 CRUMBS PROTEIN HOMOLOG 1.
FT DOMAIN 70 108 EGF-LIKE 1.
FT DOMAIN 110 146 EGF-LIKE 2.
FT DOMAIN 148 184 EGF-LIKE 3.
FT DOMAIN 186 222 EGF-LIKE 4.
FT DOMAIN 224 260 EGF-LIKE 5.
FT DOMAIN 304 337 EGF-LIKE 6.
FT DOMAIN 339 395 EGF-LIKE 7.
FT DOMAIN 441 481 EGF-LIKE 8.
FT DOMAIN 485 670 LAMININ G-LIKE 1.
FT DOMAIN 672 708 EGF-LIKE 9.
FT DOMAIN 714 885 LAMININ G-LIKE 2.
FT DOMAIN 887 923 EGF-LIKE 10.
FT DOMAIN 950 1137 LAMININ G-LIKE 3.
FT DOMAIN 1139 1175 EGF-LIKE 11.
FT DOMAIN 1177 1212 EGF-LIKE 12.
FT DOMAIN 1214 1250 EGF-LIKE 13.
FT DOMAIN 1255 1295 EGF-LIKE 14.
FT DOMAIN 1297 1333 EGF-LIKE 15.
FT DISULFID 74 85 POTENTIAL.
FT DISULFID 79 96 POTENTIAL.
FT DISULFID 98 107 POTENTIAL.
FT DISULFID 114 125 POTENTIAL.
FT DISULFID 119 134 POTENTIAL.
FT DISULFID 136 145 POTENTIAL.
FT DISULFID 152 163 POTENTIAL.
FT DISULFID 157 172 POTENTIAL.
FT DISULFID 174 183 POTENTIAL.
FT DISULFID 190 201 POTENTIAL.
FT DISULFID 195 210 POTENTIAL.
FT DISULFID 212 221 POTENTIAL.
FT DISULFID 228 239 POTENTIAL.
FT DISULFID 233 248 POTENTIAL.
FT DISULFID 250 259 POTENTIAL.
FT DISULFID 305 316 POTENTIAL.
FT DISULFID 310 325 POTENTIAL.
FT DISULFID 327 336 POTENTIAL.
FT DISULFID 343 354 POTENTIAL.
FT DISULFID 348 383 POTENTIAL.
FT DISULFID 385 394 POTENTIAL.
FT DISULFID 445 456 POTENTIAL.
FT DISULFID 450 469 POTENTIAL.
FT DISULFID 471 480 POTENTIAL.
FT DISULFID 676 687 POTENTIAL.

FT DISULFID 681 696 POTENTIAL.
FT DISULFID 698 707 POTENTIAL.
FT DISULFID 891 902 POTENTIAL.
FT DISULFID 896 911 POTENTIAL.
FT DISULFID 913 922 POTENTIAL.
FT DISULFID 1143 1154 POTENTIAL.
FT DISULFID 1148 1163 POTENTIAL.
FT DISULFID 1165 1174 POTENTIAL.
FT DISULFID 1181 1191 POTENTIAL.
FT DISULFID 1186 1200 POTENTIAL.
FT DISULFID 1202 1211 POTENTIAL.
FT DISULFID 1218 1229 POTENTIAL.
FT DISULFID 1223 1238 POTENTIAL.
FT DISULFID 1240 1249 POTENTIAL.
FT DISULFID 1259 1274 POTENTIAL.
FT DISULFID 1268 1283 POTENTIAL.
FT DISULFID 1285 1294 POTENTIAL.
FT DISULFID 1301 1312 POTENTIAL.
FT DISULFID 1306 1321 POTENTIAL.
FT DISULFID 1323 1332 POTENTIAL.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 42 42 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 322 322 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 427 427 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 550 550 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 561 561 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 657 657 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 757 757 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 871 871 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 880 880 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 968 968 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 975 975 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1000 1000 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1190 1190 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1265 1265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1273 1273 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 161 161 A -> V (IN RP12).
FT VARIANT 250 250 /FTID=VAR_011641.
FT VARIANT 745 745 C -> W (IN RP12).
FT VARIANT 745 745 /FTID=VAR_011642.
FT VARIANT 764 764 T -> M (IN RP12).
FT VARIANT 764 764 /FTID=VAR_011643.
FT VARIANT 948 948 R -> C (IN RP12).
FT VARIANT 948 948 /FTID=VAR_011644.
FT VARIANT 1041 1041 C -> Y (IN RP12).
FT VARIANT 1041 1041 /FTID=VAR_011645.
FT VARIANT 1071 1071 M -> T (IN RP12).
FT VARIANT 1071 1071 /FTID=VAR_011646.
FT VARIANT 1100 1100 L -> P (IN RP12).
FT VARIANT 1100 1100 /FTID=VAR_011647.
FT VARIANT 1181 1181 I -> R (IN LCA).
FT VARIANT 1181 1181 /FTID=VAR_011648.
FT VARIANT 1181 1181 C -> R (IN RP WITH COAT-LIKE EXUDATIVE VASCULOPATHY).
FT SQ SEQUENCE 1376 AA; 151412 MW; F380DF2AA046A2FE CRC64;

Query Match 8.4%; Score 77; DB 1; Length 1376;
Best local Similarity 23.7%; Pred. No. 6.5;
Matches 36; Conservative 19; Mismatches 45; Indels 52; Gaps 10;

QY 18 PPHY-----VSAPGTTTARWSTGLCHCFDDPANCILVTSVCPCTIFGQISELNGKTT 69
Db 99 PPGYSGTICETTIGSGRNCQHG-GICH--QDP--IYPVCICPAGYAGRFEIDHDECA 153
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FT DISULFID 399 427 BY SIMILARITY.
FT DISULFID 429 438 BY SIMILARITY.
FT DISULFID 441 451 BY SIMILARITY.
FT DISULFID 454 467 BY SIMILARITY.
FT DISULFID 456 471 BY SIMILARITY.
FT DISULFID 473 482 BY SIMILARITY.
FT DISULFID 485 500 BY SIMILARITY.
FT DISULFID 742 751 BY SIMILARITY.
FT DISULFID 744 757 BY SIMILARITY.
FT DISULFID 760 769 BY SIMILARITY.
FT DISULFID 772 788 BY SIMILARITY.
FT DISULFID 791 806 BY SIMILARITY.
FT DISULFID 793 816 BY SIMILARITY.
FT DISULFID 819 828 BY SIMILARITY.
FT DISULFID 831 846 BY SIMILARITY.
FT DISULFID 849 863 BY SIMILARITY.
FT DISULFID 851 870 BY SIMILARITY.
FT DISULFID 873 882 BY SIMILARITY.
FT DISULFID 885 899 BY SIMILARITY.
FT DISULFID 902 914 BY SIMILARITY.
FT DISULFID 904 921 BY SIMILARITY.
FT DISULFID 923 932 BY SIMILARITY.
FT DISULFID 935 948 BY SIMILARITY.
FT DISULFID 951 963 BY SIMILARITY.
FT DISULFID 953 969 BY SIMILARITY.
FT DISULFID 971 980 BY SIMILARITY.
FT DISULFID 983 995 BY SIMILARITY.
FT DISULFID 998 1007 BY SIMILARITY.
FT DISULFID 1000 1014 BY SIMILARITY.
FT DISULFID 1016 1025 BY SIMILARITY.
FT DISULFID 1028 1041 BY SIMILARITY.
FT DISULFID 1044 1056 BY SIMILARITY.
FT DISULFID 1046 1063 BY SIMILARITY.
FT DISULFID 1065 1074 BY SIMILARITY.
FT DISULFID 1077 1087 BY SIMILARITY.
FT DISULFID 1403 1412 BY SIMILARITY.
FT DISULFID 1405 1419 BY SIMILARITY.
FT DISULFID 1422 1431 BY SIMILARITY.
FT DISULFID 1434 1449 BY SIMILARITY.
FT DISULFID 1452 1466 BY SIMILARITY.
FT DISULFID 1454 1476 BY SIMILARITY.
FT DISULFID 1479 1488 BY SIMILARITY.
FT DISULFID 1491 1506 BY SIMILARITY.
FT DISULFID 1509 1521 BY SIMILARITY.
FT DISULFID 1511 1528 BY SIMILARITY.
FT DISULFID 1530 1539 BY SIMILARITY.
FT DISULFID 1542 1553 BY SIMILARITY.
FT DISULFID 1556 1566 INTERCHAIN (PROBABLE).
FT DISULFID 1560 1560 INTERCHAIN (PROBABLE).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 763 763 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 952 952 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1407 1407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1579 1579 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1678 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1689 1689 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1698 1698 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1717 1717 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1804 1804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1894 1894 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 8.3%; Score 76; DB 1; Length 3075;
Best Local Similarity 20.1%; Pred. No. 19;
Matches 32; Conservative 16; Mismatches 55; Indels 56; Gaps 9;
QY 21 YVSAPGTTTARNSTGLCHC-----FDDPANCLVTSVCPITFGQISE 62
DB 905 HVKSGHSVACHLETGLCDCKPNVTVQCQDCLHGYGLDSHGHC---RPCNCVSAGVSVD 961
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QY 63 ILNKGTTSCGRGALYCLLGLTGLPSLYSCFYRSKMRGYDLEAPCVDC-LVHV--PCE 119
DB 962 -----CTDEGQCHCVPGVAG-KRCDCAH-----GFYAYQDSCTPCDCHPTQNTCD 1008
QY 120 P-----CALCOEYRELKNGRFGDMGIGWOA 143
DB 1009 PETGECVCPHTQGGKCECED-----GHWGYDAEVCQA 1043

RESULT 14
TIE2_HUMAN
ID TIE2_HUMAN STANDARD; PRT; 1124 AA.
AC Q02763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (P140 TEK) (Tunica interna endothelial cell kinase).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R.;
RT "Molecular cloning and characterization of a novel receptor protein tyrosine kinase from human placenta.";
RL Oncogene 8:663-670(1993).
RN [2]
RP VARIANT VMC1 TRP-849.
RX MEDLINE=97134665; PubMed=8980225;
RA Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J.,
RA Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
RA Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the receptor tyrosine kinase TIE2.";
RL Cell 87:1181-1190(1996).
RN [3]
RP VARIANTS VMC1 TRP-849 AND SER-897.
RX MEDLINE=99299243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
RA Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasyk K.A.,
RA Speer M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations.";
RL Hum. Mol. Genet. 8:1279-1289(1999).
CC -!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL FORMATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
CC -!- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS MALFORMATIONS (VMC1), AN ERROR OF VASCULAR MORPHOGENESIS CHARACTERIZED BY DILATED, SERPINOUS CHANNELS.
CC -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:46:57 ; Search time 27.59 Seconds  
(without alignments)  
1022.043 Million cell updates/sec

Title: US-09-898-659-2  
Perfect score: 921  
Sequence: 1 MYPTVGYNLGLMKQPYVPPH.....NMDRSGVTMPYPYHAGMTR 163

Scoring table: ~ BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	921	100.0	163	10	Q9LKV6	Q9LKV6 lycopersico
2	899	97.6	163	10	Q9LKV7	Q9LKV7 lycopersico
3	433	47.0	152	10	Q9LQ04	Q9LQ04 arabidopsis
4	403.5	43.8	160	10	Q9SX24	Q9SX24 arabidopsis
5	403	43.8	151	10	Q9LQ02	Q9LQ02 arabidopsis
6	378	41.0	145	10	Q9ZTM8	Q9ZTM8 petunia hyb
7	365.5	39.7	224	10	Q9M9A5	Q9M9A5 arabidopsis
8	358.5	38.9	184	10	Q9LS44	Q9LS44 arabidopsis
9	347	37.7	133	10	Q9LS43	Q9LS43 arabidopsis
10	319.5	34.7	184	10	Q9LS45	Q9LS45 arabidopsis
11	299.5	32.5	161	10	Q94L14	Q94L14 oryza sativ
12	288	31.3	190	10	Q9M815	Q9M815 arabidopsis
13	270.5	29.4	174	10	Q9SX26	Q9SX26 arabidopsis
14	193	21.0	147	10	Q9SDC9	Q9SDC9 oryza sativ
15	193	21.0	238	10	Q9FPE1	Q9FPE1 arabidopsis
16	193	21.0	244	10	Q9SHD7	Q9SHD7 arabidopsis

17	166	18.0	240	10	Q9FGN2	Q9fgn2 arabidopsis
18	166	18.0	241	10	P94032	P94032 arabidopsis
19	164	17.8	242	10	Q9ZQC8	Q9zqc8 arabidopsis
20	156.5	17.0	235	10	Q9FV00	Q9fyq0 oryza sativ
21	153	16.6	525	10	Q94D92	Q94d92 oryza sativ
22	151	16.4	241	10	Q9M5D4	Q9m5d4 chlamydomon
23	135	14.7	112	11	Q9J148	Q9j148 mus musculu
24	134	14.5	115	4	Q9NZF1	Q9nzi1 homo sapien
25	132	14.3	115	4	Q96EJ4	Q96ej4 homo sapien
26	123.5	13.4	440	10	Q9ASR5	Q9asr5 arabidopsis
27	123	13.4	447	10	Q65629	Q65629 arabidopsis
28	119	12.9	111	11	Q9D7R1	Q9d7r1 mus musculu
29	118	12.8	179	4	Q9BYD5	Q9byd5 homo sapien
30	115	12.5	417	10	Q22563	Q22563 arabidopsis
31	108	11.7	253	10	Q943N4	Q943n4 oryza sativ
32	104.5	11.3	230	5	O15846	O15846 leishmania
33	95.5	10.4	777	5	Q24550	Q24550 drosophila
34	95.5	10.4	777	5	Q9V1P1	Q9vyp1 drosophila
35	94.5	10.3	641	5	Q9V7I1	Q9v7i1 drosophila
36	93.5	10.2	297	10	Q9FN61	Q9fn61 arabidopsis
37	92	10.0	790	5	Q9GSF3	Q9gsf3 podocoryne
38	91.5	9.9	177	11	Q9DAB1	Q9dab1 mus musculu
39	86.5	9.4	81	10	Q9M5D5	Q9m5d5 chlamydomon
40	85.5	9.3	229	11	Q9QZ1	Q9qz1 mus musculu
41	85.5	9.3	266	11	Q9RIK1	Q9rik1 rattus norv
42	85.5	9.3	337	11	Q9RIK0	Q9rik0 rattus norv
43	85.5	9.3	2764	11	Q9WTS5	Q9wts5 mus musculu
44	85.5	9.3	2765	11	Q9RIK2	Q9rik2 rattus norv
45	84	9.1	232	10	Q9CAJ7	Q9caj7 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q9LKV6	PRELIMINARY;	PRT;	163 AA.
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DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)			
DE	ORFX.			
OS	Lycopersicon pennellii (Tomato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxID=28526;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Frary A., Nesbitt T., Clint, Frary A., Grandillo S., van der Knaap E.,			
RA	Cong B., Liu J., Meller J., Elber R., Alpert K.B., Tanksley S.D.;			
RT	"fw2.2: a quantitative trait locus key to the evolution of tomato			
RT	fruit size."			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF261775; AAF74287.1; -.			
SQ	SEQUENCE 163 AA; 18062 MW; 0628795F184B4869 CRC64;			

Query Match	100.0%;	Score 921;	DB 10;	Length 163;
Best Local Similarity	100.0%;	Pred. NO. 1.3e-98;		
Matches 163;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MYPTVGYNLGLMKQPYVPPHYVSAGTTTARWSTGLCHCFDDPANCLVTSVCPCTITFGQI	60	
Qy	61	SEILNKGTTCGSGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEAPCVCLVHVHVFCEP	120	
Db	61	SEILNKGTTCGSGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEAPCVCLVHVHVFCEP	120	
Qy	121	CALCOEYRELKNRGFDGMIGIQAQNMNDROSGVTPPPYHAGMTR	163	
Db	121	CALCOEYRELKNRGFDGMIGIQAQNMNDROSGVTPPPYHAGMTR	163	





RESULT	6
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ID	Q9ZTM8
AC	Q9ZTM8;
PRELIMINARY;	
PRT;	145 AA.

Query Match 39.7%; Score 365.5; DB 10; Length 224;  
Best Local Similarity 41.8%; Pred. No. 3.2e-34;  
Matches 76; Conservative 29; Mismatches 48; Indels 29; Gaps







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:46:37 ; Search time 30.38 Seconds  
(without alignments)  
595.952 Million cell updates/sec

Title: US-09-898-659-2  
Perfect score: 921  
Sequence: 1 MYPTVGYNLGLMKQPVPPH.....NMDRQSGVTMPYPYHAGMTR 163

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					% Match		Query		Description	
Result No.	Score	Match	Length	ID						
1	433	47.0	152	21	AAG36900		Arabidopsis thalia			
2	425	46.1	152	21	AAG39510		Arabidopsis thalia			
3	403.5	43.8	160	21	AAG16620		Arabidopsis thalia			
4	403.5	43.8	173	21	AAG16619		Arabidopsis thalia			
5	403	43.8	151	21	AAG40342		Arabidopsis thalia			
6	363	39.4	133	21	AAG16621		Arabidopsis thalia			
7	289	31.4	190	21	AAG10515		Arabidopsis thalia			
8	289	31.4	194	21	AAG10514		Arabidopsis thalia			
9	288	31.3	188	19	AAW72391		Pathogen response			
10	280.5	30.5	190	21	AAG14719		Arabidopsis thalia			
11	280.5	30.5	190	21	AAG46457		Arabidopsis thalia			

12	231.5	25.1	90	21	AAG40343	Arabidopsis thalia
13	226	24.5	79	21	AAG40344	Arabidopsis thalia
14	211	22.9	133	21	AAG14720	Arabidopsis thalia
15	211	22.9	133	21	AAG46458	Arabidopsis thalia
16	207	22.3	76	21	AAG04523	Arabidopsis thalia
17	194	21.1	70	21	AAG36901	Arabidopsis thalia
18	193	21.0	198	21	AAG07319	Arabidopsis thalia
19	193	21.0	198	21	AAG38298	Arabidopsis thalia
20	193	21.0	244	21	AAG07318	Arabidopsis thalia
21	193	21.0	244	21	AAG38297	Arabidopsis thalia
22	170	18.5	106	21	AAG10516	Arabidopsis thalia
23	166	18.0	240	21	AAG51030	Arabidopsis thalia
24	166	18.0	241	21	AAG51029	Arabidopsis thalia
25	164	17.8	240	21	AAG10396	Arabidopsis thalia
26	164	17.8	241	21	AAG10395	Arabidopsis thalia
27	164	17.8	242	21	AAG24599	Arabidopsis thalia
28	164	17.8	242	21	AAG30353	Arabidopsis thalia
29	164	17.8	242	21	AAG49966	Arabidopsis thalia
30	140	15.2	169	21	AAG51031	Arabidopsis thalia
31	138	15.0	169	21	AAG10397	Arabidopsis thalia
32	134	14.5	115	21	AA08524	Protein encoded by
33	134	14.5	115	21	AA065397	Human 5' EST relat
34	134	14.5	115	22	AAG93299	Human protein HP10
35	134	14.5	120	21	AA053361	Human colon cancer
36	132	14.3	115	20	AA059693	Secreted protein 4
37	128	13.9	130	21	AAG07320	Arabidopsis thalia
38	128	13.9	130	21	AAG38299	Arabidopsis thalia
39	123	13.4	357	21	AAG14892	Arabidopsis thalia
40	123	13.4	357	21	AAG48943	Arabidopsis thalia
41	123	13.4	384	21	AAG14891	Arabidopsis thalia
42	123	13.4	384	21	AAG48942	Arabidopsis thalia
43	123	13.4	421	21	AAG14890	Arabidopsis thalia
44	123	13.4	421	21	AAG48941	Arabidopsis thalia
45	117.5	12.8	188	21	AAG55093	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAG36900 ID AAG36900 standard; Protein; 152 AA.

XX AC AAG36900;

XX AC AAG36900;

DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 45286.

XX DE Arabidopsis thaliana.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX XX 06-SEP-2000.

XX XX 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126284.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

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XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
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KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
OS	Arabidopsis thaliana.	
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PD	06-SEP-2000.	
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PR	14-OCT-1999;	99US-0159331.	PR	19-APR-1999;	99US-0130077.
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PR	21-OCT-1999;	99US-0159584.	PR	23-APR-1999;	99US-0130891.
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PR	22-OCT-1999;	99US-0160980.	PR	06-MAY-1999;	99US-0132487.
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PR	25-OCT-1999;	99US-0161406.	PR	14-MAY-1999;	99US-0134221.
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PR	28-OCT-1999;	99US-0161992.	PR	21-MAY-1999;	99US-0135353.
PR	28-OCT-1999;	99US-0161993.	PR	24-MAY-1999;	99US-0135629.
PR	29-OCT-1999;	99US-0162142.	PR	25-MAY-1999;	99US-0136021.
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Best Local Similarity 48.4%; Pred. No. 5.5e-35;					
Matches 75; Conservative 21; Mismatches 47; Indels 12; Gaps 4;					
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Db	4 qlhaaph-----aqgewstgfcdfadernccitlccpcttfgvaeivdrgskcca 56		PR	04-JUN-1999;	99US-0137502.
Qy	74 RQALYCLLGL-TGLPSLYSCFYRSKRCQYDLEAPCVDCLVHVFCPCALCQEVRELKN 132		PR	07-JUN-1999;	99US-0137724.
Db	57 agalymilditsecrgvacfygkmaragynikgdcgtdclkhfcfnlcaltgqyrelkh 116		PR	08-JUN-1999;	99US-0138094.
Qy	133 RCFDNGICGQANMDROSR--GVTM--PPYHAGMTR 163		PR	10-JUN-1999;	99US-0138540.
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RESULT 6					
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ID	AAG16621 standard; Protein; 133 AA.				
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AC					
DT	17-OCT-2000 (first entry)				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 17337.				
XX					
KW	Protein identification; signal transduction pathway; metabolic pathway;				
KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
XX	termination sequence.				
OS	Arabidopsis thaliana.				
XX					
PN	EPI033405-A2.				
XX					
PD	06-SEP-2000.				
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PF	25-FEB-2000; 2000EP-0301439.				
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PR 19-APR-1999; 99US-0130077.  
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PR 07-SEP-1999; 99US-0152363.  
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PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.

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Db	35	fapnpyqanvnlsgrpwstgldfcqadqanavlttiivpcvtfgqiaevmdgemtcpl 94	PR	07-JUN-1999;	99US-0137724.
Qy	74	RGALYCLLGLTGLPSLYSCF-----YRSKMRGQVDLEEAPCVDCLVHVFCPCALCQEYR 128	PR	08-JUN-1999;	99US-0138094.
Db	95	gtfmyllm---mpalcshwvmskyreknrrkfnlveapysdcashvlpcscslcqeyr 150	PR	10-JUN-1999;	99US-0138540.
Qy	129	ELKNRGFDGMIGW----QANMDRQSRGVTMPVYHAGMTR 163	PR	18-JUN-1999;	99US-0139454.
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DT	17-OCT-2000 (first entry)				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 8869.				
XX	XX				
KW	Protein identification; signal transduction pathway; metabolic pathway;				
KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
KW	termination sequence.				
XX	XX				
OS	Arabidopsis thaliana.				
XX	XX				
PN	EP1033405-A2.				
XX	XX				
PD	06-SEP-2000.				
XX	XX				
PF	25-FEB-2000; 2000EP-0301439.				
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PR 23-AUG-1999; 99US-0149930.  
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KW hybridisation assay; genetic mapping; gene expression control; promoter;  
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